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(54) Title: MODIFIED ANTI-TNF ALPHA ANTIBODY

(57) Abstract: The invention relates to the modification of antibodies reactive to human tumor necrosis factor alpha (TNF alpha) to result in anti-TNF alpha antibodies that are substantially non-immunogenic or less immunogenic than any non-modified parental antibody when used *in vivo*. The invention relates also to peptide molecules comprising T-cell epitopes of the V-regions of the parental antibody which are modified by amino acid alteration in order to reduce or eliminate said T-cell epitopes.

MODIFIED ANTI-TNF ALPHA ANTIBODY

FIELD OF THE INVENTION

The present invention relates to polypeptides to be administered especially to humans and

5   in particular for therapeutic use. The polypeptides are modified polypeptides whereby the modification results in a reduced propensity for the polypeptide to elicit an immune response upon administration to the human subject. The invention in particular relates to the modification of antibodies reactive to human tumor necrosis factor alpha (TNF alpha) to result in anti-TNF alpha antibodies that are substantially non-immunogenic or less

10   immunogenic than any non-modified counterpart when used *in vivo*.

BACKGROUND OF THE INVENTION

There are many instances whereby the efficacy of a therapeutic protein is limited by an unwanted immune reaction to the therapeutic protein. Several mouse monoclonal

15   antibodies have shown promise as therapies in a number of human disease settings but in certain cases have failed due to the induction of significant degrees of a human anti-murine antibody (HAMA) response [Schroff, R. W. et al (1985) *Cancer Res.* 45: 879-885; Shawler, D.L. et al (1985) *J. Immunol.* 135: 1530-1535]. For monoclonal antibodies, a number of techniques have been developed in attempt to reduce the HAMA response

20   [WOA8909622; EPA0239400; EPA0438310; WOA9106667; EPA0699755]. These recombinant DNA approaches have generally reduced the mouse genetic information in the final antibody construct whilst increasing the human genetic information in the final construct. Notwithstanding, the resultant "humanized" antibodies have, in several cases, still elicited an immune response in patients [Issacs J.D. (1990) *Sem. Immunol.* 2: 449,

25   456; Rebello, P.R. et al (1999) *Transplantation* 68: 1417-1420].

Antibodies are not the only class of polypeptide molecule administered as a therapeutic agent against which an immune response may be mounted. Even proteins of human origin and with the same amino acid sequences as occur within humans can still induce an

30   immune response in humans. Notable examples include therapeutic use of granulocyte-macrophage colony stimulating factor [Wadhwa, M. et al (1999) *Clin. Cancer Res.* 5: 1353-1361] and interferon alpha 2 [Russo, D. et al (1996) *Bri. J. Haem.* 94: 300-305; Stein, R. et al (1988) *New Engl. J. Med.* 318: 1409-1413] amongst others.

Key to the induction of an immune response is the presence within the protein of peptides that can stimulate the activity of T-cells via presentation on MHC class II molecules, so-called "T-cell epitopes". Such T-cell epitopes are commonly defined as any amino acid residue sequence with the ability to bind to MHC Class II molecules. Implicitly, a "T-cell

5   epitope" means an epitope which when bound to MHC molecules can be recognized by a T-cell receptor (TCR), and which can, at least in principle, cause the activation of these T-cells by engaging a TCR to promote a T-cell response.

MHC Class II molecules are a group of highly polymorphic proteins which play a central

10   role in helper T-cell selection and activation. The human leukocyte antigen group DR (HLA-DR) are the predominant isotype of this group of proteins however, isotypes HLA-DQ and HLA-DP perform similar functions. The present invention is applicable to the detection of T-cell epitopes presented within the context of DR, DP or DQ MHC Class II. In the human population, individuals bear two to four DR alleles, two DQ and two DP

15   alleles. The structure of a number of DR molecules has been solved and these appear as an open-ended peptide binding groove with a number of hydrophobic pockets which engage hydrophobic residues (pocket residues) of the peptide [Brown et al *Nature* (1993) 364: 33; Stern et al (1994) *Nature* 368: 215]. Polymorphism identifying the different allotypes of class II molecule contributes to a wide diversity of different binding surfaces

20   for peptides within the peptide binding grove and at the population level ensures maximal flexibility with regard to the ability to recognize foreign proteins and mount an immune response to pathogenic organisms.

An immune response to a therapeutic protein proceeds via the MHC class II peptide

25   presentation pathway. Here exogenous proteins are engulfed and processed for presentation in association with MHC class II molecules of the DR, DQ or DP type. MHC Class II molecules are expressed by professional antigen presenting cells (APCs), such as macrophages and dendritic cells amongst others. Engagement of a MHC class II peptide complex by a cognate T-cell receptor on the surface of the T-cell, together with

30   the cross-binding of certain other co-receptors such as the CD4 molecule, can induce an activated state within the T-cell. Activation leads to the release of cytokines further activating other lymphocytes such as B cells to produce antibodies or activating T killer cells as a full cellular immune response.

T-cell epitope identification is the first step to epitope elimination, however there are few clear cases in the art where epitope identification and epitope removal are integrated into a single scheme. Thus WO98/52976 and WO00/34317 teach computational threading approaches to identifying polypeptide sequences with the potential to bind a sub-set of

5   human MHC class II DR allotypes. In these teachings, predicted T-cell epitopes are removed by the use of judicious amino acid substitution within the protein of interest. However with this scheme and other computationally based procedures for epitope identification [Godkin, A.J. et al (1998) *J. Immunol.* 161: 850-858; Sturniolo, T. et al (1999) *Nat. Biotechnol.* 17: 555-561], peptides predicted to be able to bind MHC class II

10   molecules may not function as T-cell epitopes in all situations, particularly, *in vivo* due to the processing pathways or other phenomena. In addition, the computational approaches to T-cell epitope prediction have in general not been capable of predicting epitopes with DP or DQ restriction.

15   Besides computational techniques, there are *in vitro* methods for measuring the ability of synthetic peptides to bind MHC class II molecules. An exemplary method uses B-cell lines of defined MHC allotype as a source of MHC class II binding surface and may be applied to MHC class II ligand identification [Marshall K.W. et al. (1994) *J. Immunol.* 152:4946-4956; O'Sullivan et al (1990) *J. Immunol.* 145: 1799-1808; Robadey C. et al

20   (1997) *J. Immunol* 159: 3238-3246]. However, such techniques are not adapted for the screening multiple potential epitopes to a wide diversity of MHC allotypes, nor can they confirm the ability of a binding peptide to function as a T-cell epitope.

Recently techniques exploiting soluble complexes of recombinant MHC molecules in

25   combination with synthetic peptides have come into use [Kern, F. et al (1998) *Nature Medicine* 4:975-978; Kwok, W.W. et al (2001) *TRENDS in Immunol.* 22:583-588]. These reagents and procedures are used to identify the presence of T-cell clones from peripheral blood samples from human or experimental animal subjects that are able to bind particular MHC-peptide complexes and are not adapted for the screening multiple

30   potential epitopes to a wide diversity of MHC allotypes.

Biological assays of T-cell activation can provide a practical option to providing a reading of the ability of a test peptide/protein sequence to evoke an immune response. Examples

of this kind of approach include the work of Petra et al using T-cell proliferation assays to the bacterial protein staphylokinase, followed by epitope mapping using synthetic peptides to stimulate T-cell lines [Petra, A.M. et al (2002) *J. Immunol.* 168: 155-161]. Similarly, T-cell proliferation assays using synthetic peptides of the tetanus toxin protein

5   have resulted in definition of immunodominant epitope regions of the toxin [Reece J.C. et al (1993) *J. Immunol.* 151: 6175-6184]. WO99/53038 discloses an approach whereby T-cell epitopes in a test protein may be determined using isolated sub-sets of human immune cells, promoting their differentiation *in vitro* and culture of the cells in the presence of synthetic peptides of interest and measurement of any induced proliferation in

10   the cultured T-cells. The same technique is also described by Stickler et al [Stickler, M.M. et al (2000) *J. Immunotherapy* 23:654-660], where in both instances the method is applied to the detection of T-cell epitopes within bacterial subtilisin. Such a technique requires careful application of cell isolation techniques and cell culture with multiple cytokine supplements to obtain the desired immune cell sub-sets (dendritic cells, CD4+

15   and or CD8+ T-cells) and is not conducive to rapid through-put screening using multiple donor samples.

As depicted above and as consequence thereof, it would be desirable to identify and to remove or at least to reduce T-cell epitopes from a given in principal therapeutically

20   valuable but originally immunogenic peptide, polypeptide or protein. One of these therapeutically valuable molecules is a monoclonal antibody with binding specificity for tumor necrosis factor alpha (TNF alpha). The preferred monoclonal antibody of the present invention is a modified form of the antibody cA2 described in U.S patent No. 6,284,471. The antibody cA2 is herein referred to as the "parental" antibody of the

25   invention.

It is an objective of the invention to provide for modified forms of the parental mouse-derived monoclonal antibody with binding specificity to human TNF alpha with one or more T cell epitopes removed. TNF alpha is involved in the mediation of a number of

30   pathological conditions including Crohn's disease, rheumatoid arthritis and endotoxic or cardiovascular shock. The modified antibody of the invention can be expected to have therapeutic utility in these conditions and other diseases in which TNF alpha is a significant component of the pathophysiology.

The cA2 antibody is not the only antibody with binding specificity for TNF alpha. A variety of polyclonal and monoclonal preparations with similar specificity are known in the art. Examples include the anti-TNF alpha preparations disclosed in EP0212489, EP0218868, EP0288088 and WO91/02078. Further examples of rodent or murine

5   monoclonal antibodies specific for recombinant human TNF alpha have been described in the literature [see for example; Liang, et al (1986) *Biochem. Biophys. Res. Comm.* 137: 847-854; Meager, et al. (1987), *Hybridoma* 6: 305-311; Fendly et al. (1987), *Hybridoma* 6: 359-369; Bringman, et al (1987), *Hybridoma* 6: 489-507; Hirai, et al., (1987) *J. Immunol. Meth.* 96: 57-62 and Moller, et al (1990), *Cytokine* 2: 162-169]. Some of these

10   antibodies are able to neutralise the effect of TNF alpha *in vitro* and have been used to develop immunoassays for TNF alpha or are used in the purification of recombinant TNF alpha. In general, and in contrast with antibody cA2, these antibodies have not been developed for *in vivo* diagnostic or therapeutic uses in humans.

15   Clinical studies have however been conducted using a murine anti-TNF alpha antibody in human subjects. In fourteen patients with severe septic shock receiving a single dose of a murine anti-TNF alpha antibody seven developed a human anti-murine antibody response to the treatment, due to the immunogenicity of the therapeutic murine antibody. [Exley, A. R. et al.(1990), *Lancet* 335: 1275-1277]. Such immunogenicity can render treatment

20   ineffective in patients undergoing diagnostic or therapeutic administration of murine anti-TNF alpha antibodies.

In this regard, Adair et al [EP0927758] describe recombinant antibody molecules including antibodies with human constant region sequences and versions in which the

25   complementarity determining regions (CDRs) have been engrafted onto modified human antibody framework sequences. Such antibodies and humanized antibodies are claimed to retain specificity to human TNF alpha□ and may be used in diagnosis and therapy.

The clinical use of antibody cA2 is described by Le et al [US5,919,425] who detail

30   methods of treating TNF alpha mediated disease using cA2 which is in fact a chimeric form of an original murine monoclonal antibody designated A2. Similarly, Feldmen et al [US6,270,766] describe use of the same antibody in combination therapy with a myeloablative agent methotrexate for the treatment of arthritis and Crohn's disease.

Large clinical trials have now been conducted using this antibody, which has received the compound name "infliximab", and is traded in some territories as REMICADE. This antibody has demonstrated a degree of therapeutic efficacy in the treatment of rheumatoid arthritis and Crohn's disease has received regulatory approval for its use as in Crohn's

5   disease in the USA and in Europe. The antibody is produced by recombinant techniques and as noted above, the antibody is "chimeric" meaning that the constant region of the antibody is comprised of sequence derived from human constant region genes and the contribution of mouse derived protein sequence is therefore reduced. Despite this up to 13% of patients treated for Crohn's disease showed an immune response to the

10   therapeutic antibody [Mani R.N. et al. (1998) *Arthritis Rheum*. 41:1552-1563; Elliot M.J. et al (1994) *Lancet* 344: 1105-1110; Targan S.R. et al (1997) *N. Engl. J. Med*. 337: 1029-1035; Present D.H. et al (1999) *N. Engl. J. Med*. 340: 1398-1405].

There is therefore a need for anti-TNF alpha antibody analogues with enhanced properties

15   and especially improvements in the biological properties of the protein. In this regard, it is highly desired to provide anti-TNF alpha antibodies with reduced or absent potential to induce an immune response in the human subject. Such proteins would expect to display an increased circulation time within the human subject and would be of particular benefit in chronic or recurring disease settings such as is the case for a number of indications for

20   anti-TNF alpha antibodies. The present invention provides for modified forms of an anti-TNF alpha antibody that are expected to display enhanced properties *in vivo*.

It is a particular objective of the present invention to provide modified anti-TNF alpha antibodies in which the immune characteristic is modified by means of reduced numbers

25   of potential T-cell epitopes.

The invention discloses sequences identified within the variable region sequences of the heavy and light chains of an anti-TNF alpha antibody that are potential T cell epitopes by virtue of MHC class II binding potential.

30

The invention further discloses sequences identified within the variable region sequences of the heavy and light chains of an anti-TNF alpha antibody that are potential T cell epitopes by virtue of their ability when presented as synthetic peptides to a population of

human peripheral blood mononuclear cells (PBMC) cultured *in vitro* to induce a
proliferative response in said PBMC cells. Such information thereby has enabled the
constitution of a map of T-cell epitopes present in the said variable regions of the
antibody and has provided the critical information required for removing the T-cell

5   epitopes from the molecule.

Where others have provided anti-TNF alpha antibody molecules including chimeric
[US,5,919,425] and humanized [EP0927758] forms, none of these teachings recognize
the importance of T cell epitopes to the immunogenic properties of the protein nor have

10 been conceived to directly influence said properties in a specific and controlled way
according to the scheme of the present invention.

SUMMARY AND DESCRIPTION OF THE INVENTION
The present invention provides for a modified antibody in which the immune

15 characteristic is modified by means of reduced or removed numbers of potential T-cell
epitopes.

The preferred murine derived non-modified "parental" monoclonal antibody of the
present invention is herein referred to as antibody cA2 is described in U.S patent No.

20 6,284,471.

The present invention discloses sequences identified within the cA2 variable region
sequences of both the heavy chain and light chain that are potential T-cell epitopes by
virtue of MHC class II binding potential.

25
The invention further discloses the major regions of the antibody V-region sequence that
are immunogenic in man and thereby provides the critical information required to conduct
modification to the sequences to eliminate or reduce the immunogenic effectiveness of
these sites.

30
In one aspect, the invention provides a modified antibody molecule having specificity for
an antigen recognized by monoclonal antibody cA2 wherein one or more amino acids in

the variable region of the said cA2 antibody is substituted to reduce MHC class II
recognition of peptides derived from this region.

In another aspect, the invention provides a variant monoclonal antibody with reduced

5   immunogenic potential in humans, said variant comprising one or more amino acid
substitutions in the V-region of the cA2 antibody to eliminate or reduce peptide fragments
of the said V-region from acting as MHC class II ligands or being able to stimulate T-
cells.

10   In a further aspect of the invention, there is provided a variant monoclonal antibody with
reduced immunogenic potential in humans, said variant comprising a combination of
heavy and light chain V-regions comprising the amino acid sequences selected from
Vh1/Vk1, Vh1/Vk5, Vh1/Vk8, Vh5/Vk12, Vh8/Vk5.

15   It is most preferred to provide and antibody featuring the combination of V-region
domains Vh5/Vk12 although other combinations of V-region compositions as listed
above may be contemplated.

The sequences of the above listed Vh and Vk sequences are detailed in full in the

20   itemized summary below and as Figure 8 which also sets out the SEQ ID No assignments
as used herein.

Accordingly, the present invention provides modified anti-TNF alpha antibodies with
reduced immunogenicity in man where the modified antibodies comprise heavy and light

25   chain variable region amino acid sequences selected from SEQ ID No:1/ SEQ ID No:5,
SEQ ID No:1/ SEQ ID No:7, SEQ ID No:1/ SEQ ID No:8, SEQ ID No:3/ SEQ ID No:6
and SEQ ID No:4/ SEQ ID No:7 or combinations of amino acids having at least 70%
similarity to one or both amino acid sequences in each of the above listed pairs.

30   The sequences according to this invention designated as SEQ ID 1 – 8 are:
<u>SEQ ID No: 1 (= Vh 1)</u>
EVQLVESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAEIRSKSINSATHYAES
VKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCSRNYYGSTYDYWGQGTTLTVSS

<u>SEQ ID No: 2 (= Vh 3)</u>

EVKLEESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAEIRSKSINSATHYAES
VKGRFTISRDDSKNSLYLQMNSLKTEDTGVYYCSRNYYGSTYDYWGQGTTVTVSS

<u>SEQ ID No: 3 (= Vh 5)</u>

5   EVKLEESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAETRSKSTNSATHYAES
VKGRFTISRDDSKNSLYLQMNSLKTEDTGVYYCSRNYYGSTYDYWGQGTTVTVSS

<u>SEQ ID No: 4 (= Vh 8)</u>

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAETRSKSTNSATHYADS
VKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCSRNYYGSTYDYWGQGTLVTVSS

10   <u>SEQ ID No: 5 (= Vk 1)</u>

DIQLTQSPDTSSASPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGVPSRFSGS
GSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGSGTNVEVKR

<u>SEQ ID No: 6 (= Vk 12)</u>

DIQLTQSPDTSSASPGERASFSCRASQFVGSSIHWYQHTTNGSPRLLIKYASESMSGVPSRFSGS
15   GSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGSGTNLEVKR

<u>SEQ ID No: 7 (= Vk 5)</u>

DIQLTQSPDTSSASPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGVPSRFSGS
GSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGGGTKVEIKR

<u>SEQ ID No: 8 (= Vk 8)</u>

20   DIQLTQSPDTSSASPGERASFSCRASQFVGSSIHWYQHTTNGSPRLLIKYASESMSGVPSRFSGS
GSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGGGTKVEIKR

In summary the invention relates to the following issues:

- a monoclonal antibody V-region heavy chain termed herein Vh1, comprising, in
25   single letter code, the amino acid sequence

     EVQLVESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAEIRSKSINSATHY
     AESVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCSRNYYGSTYDYWGQGTTLTVSS;

- a monoclonal antibody V-region heavy chain termed herein Vh3, comprising, in
     single letter code, the amino acid sequence

30   EVKLEESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAEIRSKSINSATHY
     AESVKGRFTISRDDSKNSLYLQMNSLKTEDTGVYYCSRNYYGSTYDYWGQGTTVTVSS;

- a monoclonal antibody V-region heavy chain termed herein Vh5 comprising, in single
     letter code, the amino acid sequence

     EVKLEESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAETRSKSTNSATHY
35   AESVKGRFTISRDDSKNSLYLQMNSLKTEDTGVYYCSRNYYGSTYDYWGQGTTVTVSS;

- a monoclonal antibody V-region heavy chain termed herein Vh8, comprising, in single letter code, the amino acid sequence
  EVQLVESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAETRSKSTNSATHY
  ADSVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCSRNYYGSTYDYWGQGTLVTVSS;

- a monoclonal antibody V-region light chain termed herein Vk1, comprising, in single letter code, the amino acid sequence
  DIQLTQSPDTSSASPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGVPSRF
  SGSGSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGSGTNVEVKR;

- a monoclonal antibody V-region light chain termed herein Vk12, comprising, in single letter code, the amino acid sequence
  DIQLTQSPDTSSASPGERASFSCRASQFVGSSIHWYQHTTNGSPRLLIKYASESMSGVPSRF
  SGSGSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGSGTNLEVKR;

- a monoclonal antibody V-region light chain termed herein Vk5, comprising, in single letter code, the amino acid sequence
  DIQLTQSPDTSSASPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGVPSRF
  SGSGSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGGGTKVEIKR;

- a monoclonal antibody V-region light chain termed herein Vk8, comprising, in single letter code, the amino acid sequence
  DIQLTQSPDTSSASPGERASFSCRASQFVGSSIHWYQHTTNGSPRLLIKYASESMSGVPSRF
  SGSGSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGGGTKVEIKR;

- a monoclonal antibody comprising the heavy chain V-region sequence Vh1 and a the light chain sequence Vk1

- a monoclonal antibody comprising the heavy chain V-region sequence Vh1 and a the light chain sequence Vk5

- a monoclonal antibody comprising the heavy chain V-region sequence Vh1 and a the light chain sequence Vk8

- a monoclonal antibody comprising the heavy chain V-region sequence Vh5 and a the light chain sequence Vk12

- a monoclonal antibody comprising the heavy chain V-region sequence Vh8 and a the light chain sequence Vk5

- a monoclonal antibody V-region heavy chain comprising the amino acid sequence of antibody cA2 modified to contain one or more substitutions selected from the group of substitutions; M18L, K19R, V23A, I28T, I51T, I56T, S79N, A80S, V81L, T86N, D87S, R89K, L116V wherein the amino acids are identified using single letter code

and the numbering refers to the numerical position of the amino acid where the N-terminal residue equals residue 1;

- • a monoclonal antibody V-region heavy chain comprising the amino acid sequence of antibody cA2 modified to contain one or more substitutions selected from the group
5   of substitutions K3Q, E5V, M18L, K19R, V23A, I28T, S79N, A80S, V81L, T86N, D87S, R89K, G94A wherein the amino acids are identified using single letter code and the numbering refers to the numerical position of the amino acid where the N-terminal residue equals residue 1;

- • a monoclonal antibody V-region heavy chain comprising the amino acid sequence of
10 antibody cA2 modified to contain one or more substitutions selected from the group of substitutions M18L, K19R, V23A, I28T, S79N, A80S, V81L, T86N, D87S, R89K, L116V wherein the amino acids are identified using single letter code and the numbering refers to the numerical position of the amino acid where the N-terminal residue equals residue 1;

15 • a monoclonal antibody V-region heavy chain comprising the amino acid sequence of antibody cA2 modified to contain one or more substitutions selected from the group of substitutions K3Q, E5V, M18L, K19R, V23A, I28T, I51T, I56T, E64D, S79N, A80S, V81L, T86N, D87S, R89K, G94A, T115L, L116V wherein the amino acids are identified using single letter code and the numbering refers to the numerical position
20 of the amino acid where the N-terminal residue equals residue 1;

- • a monoclonal antibody V-region light chain comprising the amino acid sequence of antibody cA2 modified to contain one or more substitutions selected from the group of substitutions; L3Q, A9D, I10T, L11S, V13A, V19A, Q38H, R39T, I58V, S74T, T77S, V78L, S80A, I83A, D85T wherein the amino acids are identified using single
25 letter code and the numbering refers to the numerical position of the amino acid where the N-terminal residue equals residue 1;

- • a monoclonal antibody V-region light chain comprising the amino acid sequence of antibody cA2 modified to contain one or more substitutions selected from the group of substitutions L3Q, A9D, I10T, L11S, V13A, I58V, S74T, T77S, V78L, S80A,
30 I83A, D85T, L104V wherein the amino acids are identified using single letter code and the numbering refers to the numerical position of the amino acid where the N-terminal residue equals residue 1;

- a monoclonal antibody V-region light chain comprising the amino acid sequence of antibody cA2 modified to contain one or more substitutions selected from the group of substitutions L3Q, A9D, I10T, L11S, V13A, I58V, S74T, T77S, V78L, S80A, I83A, D85T, S100G, N103K, L104V, V106I wherein the amino acids are identified using single letter code and the numbering refers to the numerical position of the amino acid where the N-terminal residue equals residue 1;

- a monoclonal antibody V-region light chain comprising the amino acid sequence of antibody cA2 modified to contain one or more substitutions selected from the group of substitutions L3Q, A9D, I10T, L11S, V13A, Q38H, R39T, I58V, S74T, T77S, V78L, S80A, I83A, D85T, S100G, N103K, L104V, V106I wherein the amino acids are identified using single letter code and the numbering refers to the numerical position of the amino acid where the N-terminal residue equals residue 1;

- an accordingly modified antibody V-region additionally comprising a human IgG1 constant region domain and a human kappa constant region domain;

- an accordingly modified antibody able to bind TNF alpha

- an accordingly modified antibody able to provide a protective effect to WEHI164 cells grown in otherwise lethal concentrations of TNF alpha *in vitro*;

- an accordingly modified antibody able to inhibit TNF alpha stimulated production of ICAM-1 in human endothelial cells *in vitro*;

- an accordingly modified antibody able to inhibit TNF alpha stimulated production of IL-6 in human fibroblast cells *in vitro*;

- an accordingly modified antibody comprising one or more V-region domains in which the immunogenic regions have been mapped using a T-cell assay and then modified such that upon re-testing in a T-cell assay the modified protein evokes a stimulation index smaller than the parental (non-modified) molecule;

- a modified antibody molecule having the biological activity of monoclonal antibody cA2 and being substantially non-immunogenic or less immunogenic than the non-modified cA2;

- a modified antibody molecule having the same biological activity as antibody cA2 when used *in vivo*;

- an accordingly specified antibody molecule, wherein said loss of immunogenicity is achieved by removing one or more T-cell epitopes derived from the originally non-modified molecule;

Bestätigungskopie

- an accordingly specified antibody molecule, wherein said loss of immunogenicity is achieved by reduction in numbers of MHC allotypes able to bind peptides derived from said molecule;

- an accordingly specified antibody molecule, wherein one T-cell epitope is removed;

5 • an accordingly specified antibody molecule, wherein said originally present T-cell epitopes are MHC class II ligands or peptide sequences which show the ability to stimulate or bind T-cells via presentation on MHC class II;

- an accordingly specified molecule, wherein said peptide sequences are selected from the group as depicted in Figure 1;

10 • an accordingly specified molecule, wherein 1 – 9 amino acid residues, preferably one amino acid residue in any of the originally present T-cell epitopes are altered;

- an accordingly specified molecule, wherein the alteration of the amino acid residues is substitution, addition or deletion of originally present amino acid(s) residue(s) by other amino acid residue(s) at specific position(s);

15 • an accordingly specified molecule, wherein, if necessary, additionally further alteration usually by substitution, addition or deletion of specific amino acid(s) is conducted to restore biological activity of said molecule;

- an accordingly specified molecule wherein alteration is conducted at one or more residues from any or all of the string of contiguous residues of sequences (A) - (H) as

20 below wherein said sequences are derived from the cA2 antibody V-region sequence domains of the molecule and where using single letter code;

             A. = GLVQPGGSMKLSCVAS;

             B. = WVAEIRSKSINSA;

             C. = SRDDSKSAVYLQMTDLRT

25   D. = RNYYGSTYDYWGQGTTLTVSS

             E. = DILLTQSPAILSVSPGERVSF

             F. = HWYQQRTNGSPR

             G. = LIKYASESMSGIPS

             H. = DFTLSINTVESEDIADYYCQQ

30 • a peptide molecule comprising at least 9 consecutive residues from any of the sequences (A) - (H) above;

- a peptide molecule of above sharing greater than 90% amino acid identity with any of the peptide sequences derived from (A) - (H);

- a peptide molecule of above sharing greater than 80% amino acid identity with any of the peptide sequences derived from (A) - (H) above;

- a peptide molecule containing a sequence element identical or substantially homologous with one or more of the sequences (A) - (H) above;

- peptide sequences as above able to bind MHC class II;

- a pharmaceutical composition comprising any of the peptides or modified peptides of above having the activity of binding to MHC class II

- a DNA sequence or molecule which codes for any of said specified modified molecules as defined above and below;

- a pharmaceutical composition comprising a modified molecule having the biological activity of cA2;

- a pharmaceutical composition as defined above and / or in the claims, optionally together with a pharmaceutically acceptable carrier, diluent or excipient;

- a method for manufacturing a modified molecule having the biological activity of antibody cA2 as defined above or below and comprising the following steps: (i) determining the amino acid sequence of the polypeptide or part thereof; (ii) identifying one or more potential T-cell epitopes within the amino acid sequence of the protein by any method including determination of the binding of the peptides to MHC molecules using *in vitro* or *in silico* techniques or biological assays; (iii) designing new sequence variants with one or more amino acids within the identified potential T-cell epitopes modified in such a way to substantially reduce or eliminate the activity of the T-cell epitope as determined by the binding of the peptides to MHC molecules using *in vitro* or *in silico* techniques or biological assays; (iv) constructing such sequence variants by recombinant DNA techniques and testing said variants in order to identify one or more variants with desirable properties; and (v) optionally repeating steps (ii) – (iv);

- an accordingly specified method, wherein step (iii) is carried out by substitution, addition or deletion of 1 – 9 amino acid residues in any of the originally present T-cell epitopes;

- an accordingly specified method, wherein the alteration is made with reference to an homologous protein sequence and / or *in silico* modelling techniques;

- a peptide sequence consisting of at least 9 consecutive amino acid residues of a 13mer T-cell epitope peptide as specified above and its use for the manufacture of an anti-TNF alpha antibibody having substantially no or less immunogenicity than any non-

modified molecule and having the biological activity of an anti-TNF alpha antibody when used *in vivo*.

Reference to "substantially non-immunogenic" or "reduced immunogenic potential"
includes reduced immunogenicity compared to a parent antibody, i.e. a non-modified murine or chimeric monoclonal antibody. The term "immunogenicity" includes an ability to provoke, induce or otherwise facilitate a humoral and or T-cell mediated response in a host animal and in particular where the "host animal" is a human.

10   An important and significant feature of the modified antibodies of the present is that they retain the functional activities of the non-modified or "parental" antibody. It is therefore particularly desired to produce modified antibodies in which all of the beneficial technical features associated with the therapeutic efficacy of the parental non-modified antibody are exhibited. This is pertinent to the contemplated utility of the invention, namely to provide
15   a composition with therapeutic efficacy in a number of important diseases in man including especially rheumatoid arthritis and Crohn's disease and a number of other clinical indications mediated by TNF alpha. Such a therapeutic is a preferred embodiment of the present invention.

20   Accordingly, the modified antibody of the present exhibits an affinity for its target antigen that is similar to the affinity exhibited by monoclonal antibody cA2. The antibody recognizes TNF alpha but not TNF alpha and is capable of neutralizing TNF alpha activity in a range of *in vitro* assays. Such assays include cell cytotoxicity, mitogenesis, cytokine induction and induction of adhesion molecules. In addition to
25   neutralizing the biological activity of TNF alpha, the therapeutic efficacy of the parental molecule is believed also to be mediated by the ability of the antibody to induce antibody-dependent cell mediated cytoxicity (ADCC) and is effective at killing cells expressing cell surface bound forms of TNF alpha. The phenomenon of ADCC is mediated by the constant region domain of whole antibody molecules, and the present invention
30   contemplates production of a whole antibody molecules comprising a constant region domain compatible with ADCC induction.

Bestätigungskopie

In regard to *in vitro* assays demonstrating TNF alpha neutralizing activity a number of such assays are described herein as experimental examples and provide evidence that the preferred antibodies of the invention have *in vitro* potency.

5 By "antibody" is meant a protein of the immunoglobulin family that is capable of combining, interacting or otherwise associating with an antigen. The term "antigen" is used herein to refer to a substance that is capable of interacting with the antibody and in the context of the present invention is meant to be TNF alpha. The TNF alpha of the present invention is tumor necrosis factor alpha (TNF alpha) and is most preferably

10 human TNF alpha or any TNF alpha representing an antigen for antibody cA2. The TNF alpha may be soluble TNF alpha or membrane associated TNF alpha.

The term "immunoglobulin" is used herein to refer to a protein consisting of one or more polypeptides substantially encoded by immunoglobulin genes. The recognized

15 immunoglobulin genes include the κ, λ, α, γ (IgG1, IgG2, IgG3, IgG4), σ,ε and μ constant region genes and in nature multiple immunoglobulin variable region genes. One natural form of immunoglobulin is a tetramer comprising two identical pairs in which each pair has one light chain and one heavy chain. In each pair the heavy and light chain variable regions together provide the binding surface capable of interacting with the

20 antigen. The term Vh is used herein to refer to the heavy chain variable region, and the term Vk is used herein to refer to the light chain variable region and in this instance in common with numerous monoclonal antibodies the light chain is a "kappa" (κ) type chain.

As used herein, Vh means a polypeptide that is about 110 to 125 amino acid residues in

25 length, the sequence of which corresponds to any of the specified Vh chains herein which in combination with a Vk are capable of binding human TNF alpha. Similarly, Vk means a polypeptide that is about 95-130 amino acid residues in length the sequence of which corresponds to any of the specified Vk chains herein which in combination with a Vh are capable of binding human TNF alpha. Full-length immunoglobulin heavy chains are

30 about 50 kDa molecular weight and are encoded by a Vh gene at the N-terminus and one of the constant region genes (e.g. γ) at the C-terminus. Similarly, full-length light chains are about 25 kDa molecular weight and are encoded by a V-region gene at the N-terminus and a κ or λ constant region gene at the C-terminus.

Bestätigungskopie

In addition to whole antibody (tetramers), immunoglobulins may exist in a number of
other forms derived by application of recombinant DNA techniques or protein
biochemistry. These forms include for example Fv, Fab, Fab' and (Fab)2 molecules and
could all contain any of the Vh or Vk sequences of the present invention. A further

5   example may include a "bi-specific" antibody, that is comprising a Vh/Vk combination of
the present invention in combination with a second Vh/Vk combination with a different
antigen specificity.

The term "T-cell epitope" means according to the understanding of this invention an
10 amino acid sequence which is able to bind MHC class II, able to stimulate T-cells and / or
also to bind (without necessarily measurably activating) T-cells in complex with MHC
class II.

The term "peptide" as used herein and in the appended claims, is a compound that
15 includes two or more amino acids. The amino acids are linked together by a peptide bond
(defined herein below). There are 20 different naturally occurring amino acids involved in
the biological production of peptides, and any number of them may be linked in any order
to form a peptide chain or ring. The naturally occurring amino acids employed in the
biological production of peptides all have the L-configuration. Synthetic peptides can be
20 prepared employing conventional synthetic methods, utilizing L-amino acids, D-amino
acids, or various combinations of amino acids of the two different configurations. Some
peptides contain only a few amino acid units. Short peptides, e.g., having less than ten
amino acid units, are sometimes referred to as "oligopeptides". Other peptides contain a
large number of amino acid residues, e.g. up to 100 or more, and are referred to as
25 "polypeptides". By convention, a "polypeptide" may be considered as any peptide chain
containing three or more amino acids, whereas a "oligopeptide" is usually considered as a
particular type of "short" polypeptide. Thus, as used herein, it is understood that any
reference to a "polypeptide" also includes an oligopeptide. Further, any reference to a
"peptide" includes polypeptides, oligopeptides, and proteins. Each different arrangement
30 of amino acids forms different polypeptides or proteins. The number of polypeptides–and
hence the number of different proteins–that can be formed is practically unlimited.
"Alpha carbon (Cα)" is the carbon atom of the carbon-hydrogen (CH) component that is
in the peptide chain. A "side chain" is a pendant group to Cα that can comprise a simple

or complex group or moiety, having physical dimensions that can vary significantly compared to the dimensions of the peptide.

The general method of the present invention leading to the modified anti-TNF alpha antibody comprises the following steps:

    (a) Determining the amino acid sequence of the polypeptide or part thereof

    (b) Identifying one or more potential T cell epitopes within the amino acid sequence of the protein by any method including determination of the binding of the peptides to MHC molecules using *in vitro* or *in silico* techniques or biological assays.

    (c) Designing new sequence variants with one or more amino acids within the identified potential T cell epitopes modified in such a way to substantially reduce or eliminate the activity of the T cell epitope as determined by the binding of the peptides to MHC molecules using *in vitro* or *in silico* techniques or biological assays. Such sequence variants are created in such a way to avoid creation of new potential T cell epitopes by the sequence variations unless such new potential T cell epitopes are, in turn, modified in such a way to substantially reduce or eliminate the activity of the T cell epitope.

    (d) Constructing such sequence variants by recombinant DNA techniques and testing said variants in order to identify one or more variants with desirable properties.

The identification of potential T-cell epitopes according to step (b) can be carried out according to methods described previously in the art. Suitable methods are disclosed in WO 98/59244; WO 98/52976; WO 00/34317.

Another very efficacious method for identifying T-cell epitopes by calculation is described in the Example 1, which is a preferred embodiment according to this invention. The analysis has been conducted on both the heavy chain and light chain variable region sequences of the anti-TNF alpha antibody.

A further technical approach suitable to the detection of T-cell epitopes is via biological T-cell assay. Such an analysis is described in the Example 2 and is similarly a preferred embodiment according to this invention. Accordingly, the preferred method of biological

assay embodied herein comprises the testing of overlapping peptides derived from the heavy chain and light chain variable region sequences of the anti-TNF alpha antibody or alternatively a sub-set of V-region derived peptides such as all or some of those derived by calculation according to the method embodied by Example 1. The synthetic peptides

5   are tested for their ability to evoke a proliferative response in human T-cells cultured *in vitro*. The proliferative response can be measured by any convenient means but a widely known method as exploited in the present embodiment uses ^{3}H-thymidine incorporation. This approach can be conducted using naïve human T-cells taken from healthy donors, and may also be used to test the immunogenicity in vitro of whole protein molecules as

10   well as synthetic peptides. Such a scheme has also been used in the present study (Example 11) to demonstrate to reduced immunogenic potential of a preferred molecule of the invention. The inventors have established that in the operation of a naïve T-cell assay, a stimulation index equal to or greater than 2.0 is a useful measure of induced proliferation. The stimulation index is conventionally derived by division of the

15   proliferation score measured (e.g. counts per minute if using ^{3}H-thymidine incorporation) to the test peptide, by the proliferation score measured in cells not contacted with a test (poly)peptide.

In practice a number of variant anti-TNF alpha antibodies may be produced and tested for

20   the desired immune and functional characteristic. It is particularly important when conducting alterations to the protein sequence that the contemplated changes do not introduce new immunogenic epitopes. This event is avoided in practice by re-testing the contemplated sequence for the presence of epitopes and or of MHC class II ligands by any suitable means. One particular means, which is a further embodiment of the

25   invention, is use of an *in vitro* immunological recall assay involving PBMC preparations cultured in the presence of a priming quantity of test protein (antibody) and re-challenge with either the same test protein or in parallel a modified version of the protein. Such a scheme provides a convenient practical demonstration of a reduced immunogenic potential in a modified protein in the absence of full-scale clinical trials. For most

30   purposes, the variant proteins will be produced by recombinant DNA techniques although other procedures including chemical synthesis may be contemplated.

In a particularly preferred embodiment, the modified antibodies of the present invention are generated by expression of different combinations of the Vh and Vk genes specified herein. The most preferred combination according to the invention comprises the combination Vh5 / Vk12. Other combinations have been produced and tested for

5 functional activity in binding TNF alpha and these combinations comprise Vh1 / Vk1, Vh1 / Vk5, Vh1 / Vk8 and Vh8 / Vk5. All such combinations of heavy and light chain are encompassed by the present invention.

Accordingly, the present invention provides modified anti-TNF alpha antibodies with

10 reduced immunogenicity in man where the modified antibodies comprise heavy and light chain variable region amino acid sequences selected from SEQ ID No:1/ SEQ ID No:5, SEQ ID No:1/ SEQ ID No:7, SEQ ID No:1/ SEQ ID No:8, SEQ ID No:3/ SEQ ID No:6 and SEQ ID No:4/ SEQ ID No:7 or combinations of amino acids having at least 70% similarity to one or both amino acid sequences in each of the above listed pairs.

15

The invention relates to an anti-TNF alpha monoclonal antibody in which substitutions of at least one amino acid residue have been made at positions within the V-regions of the molecule to result in a substantial reduction in activity of or elimination of one or more potential T-cell epitopes from the protein. It is most preferred to provide modified

20 antibody molecules in which amino acid modification (e.g. a substitution) is conducted within the most immunogenic regions of the parent molecule. The major preferred embodiments of the present invention comprise modified antibody molecules for which any of the MHC class II ligands are altered such as to eliminate binding or otherwise reduce the numbers of MHC allotypes to which the peptide can bind. The inventors have

25 discovered and herein disclose, the immunogenic regions of the antibody cA2 molecule in man. It is understood that under certain circumstances additional regions of sequence to those disclosed herein can become immunogenic epitopes, for example in the event of infection with a pathogen expressing a protein or peptide with a similar sequence to that of the present case. In any event, it will be critical for the

30 sequence element to act as an MHC class II ligand and in principle therefore any of the sequences disclosed in Figure 1 can be considered immunogenic epitopes under the scope of the present invention.

For the elimination of T-cell epitopes, amino acid substitutions are made at appropriate points within the peptide sequence predicted to achieve substantial reduction or elimination of the activity of the T-cell epitope. In practice an appropriate point will preferably equate to an amino acid residue binding within one of the pockets provided
5 within the MHC class II binding groove.

It is most preferred to alter binding within the first pocket of the cleft at the so-called P1 or P1 anchor position of the peptide. The quality of binding interaction between the P1 anchor residue of the peptide and the first pocket of the MHC class II binding groove is
10 recognized as being a major determinant of overall binding affinity for the whole peptide. An appropriate substitution at this position of the peptide will be for a residue less readily accommodated within the pocket, for example, substitution to a more hydrophilic residue. Amino acid residues in the peptide at positions equating to binding within other pocket regions within the MHC binding cleft are also considered and fall under the scope of the
15 present.

It is understood that single amino acid substitutions within a given potential T cell epitope are the most preferred route by which the epitope may be eliminated. Combinations of substitution within a single epitope may be contemplated and for example can be
20 particularly appropriate where individually defined epitopes are in overlap with each other. Moreover, amino acid substitutions either singly within a given epitope or in combination within a single epitope may be made at positions not equating to the "pocket residues" with respect to the MHC class II binding groove, but at any point within the peptide sequence. All such substitutions fall within the scope of the present.
25

In as far as this invention relates to modified anti-TNF alpha antibodies, compositions containing such modified antibodies or fragments of modified antibodies and related compositions should be considered within the scope of the invention. The invention therefore contemplates the use and generation of antibody fragments including for
30 example Fv, Fab, Fab' and F(ab')2 fragments. Such fragments may be prepared by standard methods [for example; Coligan et al (*Current Protocols in Immunology*, John Wiley & Sons 1991-1997]. The present invention also contemplates the various recombinant forms of antibody derived molecular species well known in the art. Such

species include stabilised Fv fragments including single chain Fv forms (e.g. scFv) comprising a peptide linker joining the Vh and Vl domains, or an Fv stabilised by interchain di-sulphide linkage (dsFv) and which contain additional cysteine residues engineered to facilitate the conjoining of the Vh and Vl domains. Equally, other

5   compositions are familiar in the art and could include species referred to as "minibodies"; and single variable domain "dAbs". Other species still may incorporate means for increasing the valency of the modified antibody V-region domain, i.e. species having multiple antigen binding sites for example by the engineering of dimerisation domains (e.g. "leucine zippers") or also chemical modification strategies.

10

In another aspect, the present invention relates to nucleic acids encoding modified anti-TNF alpha antibody entities.

In a further aspect the present invention relates to methods for therapeutic treatment of

15   humans using the modified anti-TNF alpha antibody.

The invention will now be illustrated, but not limited, by the following examples. The examples refer to the following drawings:

Figure 1 provides tables of peptide sequences derived from the V-region domain of anti-

20   TNF alpha antibody cA2 with potential human MHC class II binding activity. Figure 1A relates to heavy-chain derived sequences. Figure 1B relates to light-chain derived sequences.

Figure 2 provides a graph demonstrating the neutralization of TNF alpha induced killing of WEHI cells in vitro using an anti-TNF alpha antibody (Vh5/Vk12) of the invention.

25   Figure 3 provides a graph demonstrating the neutralization of TNF alpha stimulated production of ICAM-1 expression in human umbilical vein endothelial cells in vitro using an anti-TNF alpha antibody (Vh5/Vk12) of the invention.

Figure 4 provides a graph demonstrating the ability of an anti-TNF alpha antibody of the invention (Vh5/Vk12) to compete for binding to TNF alpha with a positive control

30   antibody (infliximab) in an in vitro assay.

Figure 5 provides a panel of histrograms representing the proliferation response to synthetic peptides in an in vitro naïve T-cell proliferation assay. The data relate to the responses recorded by PBMC from individual donor #4 and are presented for each of

peptides CA1 –CA75 at both 1μM and 5μM concentration. The graphs each plot the Stimulation Index (SI) versus the peptide identification number. SI = CPM Test Peptide/CPM untreated control. Peptide sequences and methods are detailed in Example 2.

5   **Figure 6** provides proliferative response recorded to each of the 13-mer peptides P1-P15 in an *in vitro* naïve T-cell proliferation assay. Panel A depicts responses in PBMC from donor #2; panel B depicts responses in PBMC from donor #4. The results are shown for the peptides given at both 1μM and 5μM concentration. For both panels, responses with an SI > 2.0 are indicated as positive (+) and results with an SI < 2.0 are indicated as

10   negative (-).

Figure 7 shows results of a plate ELISA in which TNF alpha is detected by the modified antibody of the invention (Vh5/Vk12). The binding curve is a plot of the antibody concentration versus optical density at 492nm (OD492).

Figure 8 provides amino acid sequences of the modified variable region domains of the

15   anti-TNF alpha antibodies of the invention. Sequences are depicted using single letter code.

Figure 9 provides a graph demonstrating the neutralization of TNF alpha stimulated production of IL-6 expression in human HS27 fibroblast cells *in vitro* using an anti-TNF alpha antibody (Vh5/Vk12) of the invention. The negative control (210G12) is a non-

20   TNF alpha binding antibody and the positive control (infliximab) is TNF alpha neutralizing.

Figure 10 provide a plots depicting the results of an immunogenicity assay using naïve human PBMC cultured in the presence of differing concentrations of modified antibody (Vh5/Vk12) or immunogenic parental antibody (infliximab). The graphs show the results

25   from a responsive donor PBMC (panel A) and non-responsive donor PBMC (panel B). SI = stimulation index

EXAMPLE 1

Identification of Potential MHC class II ligands in anti-TNF alpha VH and VL protein

30   *sequence by computational means.*

The scheme for the analysis of peptide sequences with potential to act as MHC class II binding ligands has been described in detail previously [WO 02/069232]. A software tool using this procedure has been developed and applied to the analysis of the anti-TNF alpha

antibody V-region domains. In brief, the software was built from a number of elements including a library of model MHC class II molecules, produced to cover a wide number of allotypic variants extant in the human population; a library of peptide backbone structures, produced to encompass theoretical and known backbone conformations.

5   Using these elements, a large data set was generated based on the results of docking each backbone conformation within each model MHC allotype binding groove. The data set encompasses also the best side-chain conformation for all possible amino acids at the given position. The interatomic distances between the peptide side-chains (in the optimum conformation) and the MHC protein are stored in this dataset. A test peptide

10 from the protein of interest is analysed by adding its sequence of side-chains to all backbones and then retrieving the data sets for the optimum side-chain conformations and thus calculating a "peptide score" for each backbone. The best score is selected for display and the process repeated for each of the available MHC model structures. The algorithm has been applied to the analysis of the V-region domains of the anti-TNF

15 alpha antibody cA2. The analysis identifies multiple 13mer peptide sequences which are potential T-cell epitopes by their being predicted MHC class II ligands for one or more allotypes. These peptides are shown in Figure 1A (heavy-chain derived peptides) and 1B (light-chain derived peptides).

20 **EXAMPLE 2**

Identification of T-cell epitopes using synthetic peptides and naïve human PBMC in vitro proliferation assays.

The interaction between MHC, peptide and T-cell receptor (TCR) provides the structural basis for the antigen specificity of T-cell recognition. T-cell proliferation assays test the

25 binding of peptides to MHC and the recognition of MHC/peptide complexes by the TCR. *In vitro* T-cell proliferation assays of the present example, involve the stimulation of peripheral blood mononuclear cells (PBMCs), containing antigen presenting cells (APCs) and T-cells. Stimulation is conducted *in vitro* using synthetic peptide antigens, and in some experiments whole protein antigen. Stimulated T-cell proliferation is measured

30 using ^{3}H-thymidine (^{3}H-Thy) and the presence of incorporated ^{3}H-Thy assessed using scintillation counting of washed fixed cells.

Table 1: Synthetic Peptides

Heavy chain peptides		Light chain peptides	
Peptide #	Peptide Sequence	Peptide #	Peptide Sequence
CA1	EVKLEESGGGLVQPG	CA41	DILLTQSPAILSVSP
CA2	LEESGGGLVQPGGSM	CA42	LTQSPAILSVSPGER
CA3	SGGGLVQPGGSMKLS	CA43	SPAILSVSPGERVSF
CA4	GLVQPGGSMKLSCVA	CA44	ILSVSPGERVSFSCR
CA5	QPGGSMKLSCVASGF	CA45	VSPGERVSFSCRASQ
CA6	GSMKLSCVASGFIFS	CA46	GERVSFSCRASQFVG
CA7	KLSCVASGFIFSNHW	CA47	VSFSCRASQFVGSSI
CA8	CVASGFIFSNHWMNW	CA48	SCRASQFVGSSIHWY
CA9	SGFIFSNHWMNWVRQ	CA49	ASQFVGSSIHWYQQR
CA10	IFSNHWMNWVRQSPE	CA50	FVGSSIHWYQQRTNG
CA11	NHWMNWVRQSPEKGL	CA51	SSIHWYQQRTNGSPR
CA12	MNWVRQSPEKGLEWV	CA52	HWYQQRTNGSPRLLI
CA13	VRQSPEKGLEWVAEI	CA53	QQRTNGSPRLLIKYA
CA14	SPEKGLEWVAEIRSK	CA54	TNGSPRLLIKYASES
CA15	KGLEWVAEIRSKSIN	CA55	SPRLLIKYASESMSG
CA16	EWVAEIRSKSINSAT	CA56	LLIKYASESMSGIPS
CA17	AEIRSKSINSATHYA	CA57	KYASESMSGIPSRFS
CA18	RSKSINSATHYAESV	CA58	SESMSGIPSRFSGSG
CA19	SINSATHYAESVKGR	CA59	MSGIPSRFSGSGSGT
CA20	SATHYAESVKGRFTI	CA60	IPSRFSGSGSGTDFT
CA21	HYAESVKGRFTISRD	CA61	RFSGSGSGTDFTLSI
CA22	ESVKGRFTISRDDSK	CA62	GSGSGTDFTLSINTV
CA23	KGRFTISRDDSKSAV	CA63	SGTDFTLSINTVESE
CA24	FTISRDDSKSAVYLQ	CA64	DFTLSINTVESEDIA
CA25	SRDDSKSAVYLQMTD	CA65	LSINTVESEDIADYY
CA26	DSKSAVYLQMTDLRT	CA66	NTVESEDIADYYCQQ
CA27	SAVYLQMTDLRTEDT	CA67	ESEDIADYYCQQSHS
CA28	YLQMTDLRTEDTGVY	CA68	DIADYYCQQSHSWPF
CA29	MTDLRTEDTGVYYCS	CA69	DYYCQQSHSWPFTFG
CA30	LRTEDTGVYYCSRNY	CA70	CQQSHSWPFTFGSGT
CA31	EDTGVYYCSRNYYGS	CA71	SHSWPFTFGSGTNLE

CA32	GVYYCSRNYYGSTYD	CA72	WPFTFGSGTNLEVKR
CA33	YCSRNYYGSTYDYWG	CA73	TFGSGTNLEVKRTVA
CA34	RNYYGSTYDYWGQGT	CA74	SGTNLEVKRTVAAPS
CA35	YGSTYDYWGQGTTLT	CA75	NLEVKRTVAAPSVFI
CA36	TYDYWGQGTTLTVSS		
CA37	YWGQGTTLTVSSAST		
CA38	QGTTLTVSSASTKGP		
CA39	TLTVSSASTKGPSVF		
CA40	VSSASTKGPSVFPLA		

Buffy coats from human blood stored for less than 12 hours were obtained from the National Blood Service (Addenbrooks Hospital, Cambridge, UK). Ficoll-paque was obtained from Amersham Pharmacia Biotech (Amersham, UK). Serum free AIM V

5   media for the culture of primary human lymphocytes and containing L-glutamine, $50\mu g/ml$ streptomycin, $10\mu g/ml$ gentomycin and 0.1% human serum albumin was from Gibco-BRL (Paisley, UK). Synthetic peptides were obtained from Euroséquence (Groningen, The Netherlands) and Babraham Technix (Cambridge, UK). Erythrocytes and leukocytes were separated from plasma and platelets by gentle

10   centrifugation of buffy coats. The top phase (containing plasma and platelets) was removed and discarded. Erythrocytes and leukocytes were diluted 1:1 in phosphate buffered saline (PBS) before layering onto 15ml ficoll-paque (Amersham Pharmacia, Amersham UK). Centrifugation was done according to the manufacturers recommended conditions and PBMCs were harvested from the serum+PBS/ficoll paque interface.

15   PBMCs were mixed with PBS (1:1) and collected by centrifugation. The supernatant was removed and discarded and the PBMC pellet resuspended in 50ml PBS. Cells were again pelleted by centrifugation and the PBS supernatant discarded. Cells were resuspended using 50ml AIM V media and at this point counted and viability assessed using trypan blue dye exclusion. Cells were again collected by centrifugation and the supernatant

20   discarded. Cells were resuspended for cryogenic storage at a density of 3×10^{7} per ml. The storage medium was 90%(v/v) heat inactivated AB human serum (Sigma, Poole, UK) and 10%(v/v) DMSO (Sigma, Poole, UK). Cells were transferred to a regulated freezing container (Sigma) and placed at $-70°C$ overnight. When required for use, cells were

thawed rapidly in a water bath at 37°C before transferring to 10ml pre-warmed AIM V medium.

PBMC were stimulated with protein and peptide antigens in a 96 well flat bottom plate at a density of $2x10^5$ PBMC per well. PBMC were incubated for 7 days at 37°C before

5 pulsing with ^{3}H-Thy (Amersham-Phamacia, Amersham, UK). For the present study, synthetic peptides (15mers) spanning the entire V-region domains of both the heavy chain and light chain of antibody cA2 were produced. Each peptide overlapped each successive peptide in the sequence by 12 residues, i.e., each peptide incremented from the next in the sequence by 3 residues. The peptide sequences and identification numbers are shown in

10 Table 1. Each peptide was screened individually against PBMC's isolated from 20 naïve donors. Two control peptides C32 (PKYVKQNTLKLAT) and C49 (KVVDQIKKISKPVQH) that have previously been shown to be immunogenic and a potent non-recall antigen KLH were used in each donor assay. Peptides were dissolved in DMSO to a final concentration of 10mM, these stock solutions were then diluted 1/500 in AIM V media

15 (final concentration 20μM). Peptides were added to a flat bottom 96 well plate to give a final concentration of 2 and 10μM in a 100μl. The viability of thawed PBMC's was assessed by trypan blue dye exclusion, cells were then resuspended at a density of $2x10^6$ cells/ml, and 100μl ($2x10^5$ PBMC/well) was transferred to each well containing peptides. Triplicate well cultures were assayed at each peptide concentration. Plates were

20 incubated for 7 days in a humidified atmosphere of 5% CO_2 at 37°C. Cells were pulsed for 18-21 hours with 1μCi ^{3}H-Thymidine per well before harvesting onto filter mats. CPM values were determined using a Wallac microplate beta top plate counter (Perkin Elmer). Results were expressed as stimulation indices (SI), where SI = CPM Test Peptide/CPM untreated control.

25 Mapping T cell epitopes in the cA2 V-region sequences using the naïve T cell proliferation assay resulted in the identification of several immunogenic regions. Peptides with significant stimulation indices in individual donors include for example CA34 (SI= 2.22) and CA52 (SI=2.09) amongst others.

The map was refined in sequence regions surrounding the complementarity determining

30 regions (CDRs) for the Vh and the Vk sequences using a further sub-set of 15 different 13-mer peptides (P1 - P15) with sequences as below:

     P1 = KGLEWVAEIRSKS
     P2 = EWVAEIRSKSINS

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P3  = AEIRSKSINSATH
P4  = KSINSATHYAESV
P5  = TGVYYCSRNYYGS
P6  = STYDYWGQGTTLT
P7  = SQFVGSSIHWYQQ
P8  = QFVGSSIHWYQQR
P9  = SSIHWYQQRTNGS
P10 = HWYQQRTNGSPRL
P11 = PRLLIKYASESMS
P12 = RLLIKYASESMSG
P13 = LLIKYASESMSGI
P14 = IKYASESMSGIPS
P15 = ESMSGIPSRFSGS
```

Peptides P1-P7 derive from the Vh chain sequence and peptides P8 – P15 derive from the Vk chain sequence. Peptides P1-P15 were screened for their ability to evoke an *in vitro* proliferative response in a further panel of 10 naïve PBMC preparations encompassing multiple different MHC allotypes as previously. The results of the naïve T-cell proliferation assay from both sets of synthetic peptides and donor panels can be taken together to produce an epitope map of the Vh and Vk chains of the antibody. In general, in compilation of such a map, an SI > 1.95 is taken as a positive response. Representative histograms showing the SI to all 15-mer peptides for one responsive donor is given in the accompanying FIGURE 5. Exemplary results to the 13-mer peptides P1 - P15 are given as FIGURE 6.

EXAMPLE 3

Construction of anti-TNF alpha antibody Vh and Vk genes.

The sequence of the antibody was derived from US patent 5,656,272. The Variable domain heavy chain (Vh) and the variable domain light chain (Vk) genes were made by gene synthesis. Briefly, a panel of synthetic oligonucleotides were designed and synthesised. The genes were assembled using a ligase chain reaction (LCR) wherein the oligonucleotides featuring complementary ends were allowed to anneal followed by amplification and fill-in using a polymerase chain reaction (PCR). The PCR was driven by addition of an increased concentration of the flanking oligonuclotides to act as primers. The PCR products were assembled into full-length antibody genes by further PCR from vectors containing 5' and 3' immunoglobulin gene flanking regions and sub-

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cloning into expression vectors for expression of whole antibody. The assembled Vh and
Vk genes served as templates for mutagenesis and construction of multiple variant
antibody sequences in which T-cell epitopes had been removed.

For assembly of the Vh gene oligonucleotides OL373-OL391 detailed in Table 2 were
used. For assembly of the Vk gene oligonucleotides OL392-OL410 detailed in Table 3
were used. For both genes, the LCR was conducted by mixing 20μl of phosphorylated
oligonucleotides with 1μl Pfu DNA ligase (Stratagene, Amsterdam, NL), 10 μl 10X
reaction buffer (supplied with enzyme) and 69 μl water. The reaction mix was placed in a
thermal cycler for incubation at 95 °C for 2 minutes followed by 25 cycles of 95°C for 30
seconds followed by gradual cooling to 60° then incubation at 60°C for 20 minutes and a
final incubation of 3 hours at 60°C. Typically, analysis of a sample of the LCR using 2%
agarose gel electrophoresis gave smear with a faint band of correct size just visible. The
oligonucleotides in all cases were from were from MWG-Biotech (Ebersberg, Germany)
and were phosphorylated *in vitro* using T4 DNA kinase (Roche, Lewes, UK) and the
suppliers recommended protocol. Following LCR, 5μL of the reaction was transferred to
a PCR mix to amplify the assembled fragment. Oligonucleotides OL373 and OL382
were used to drive the Vh reaction, with oligocucleotides OL392 and OL401 used to drive
the Vk reaction. PCR was conducted in a total volume of 50μl for 15 cycles using Taq
DNA polymerase (Roche, Lewes, UK). The reaction was run on a 1% agarose gel and
the desired band removed and purified using a Qiagen (Crawley, UK) DNA extraction kit.
Products were direct cloned into the pGemT-easy vector (Promega, Southampton, UK)
for sequence analysis. Several clones were sequenced until correct clones were obtained.
Full-length immunoglobulin genes containing the variable region cassettes produced as
described above were assembled using overlapping PCR. Briefly, DNA of the vectors
M13-VHPCR1 and M13-VKPCR1 [Orlandi et al (1989), *PNAS*, 89: 3833-7] were used as
templates to produce a further two overlapping PCR fragments for each Vh and Vk chains
including 5' flanking sequence with the murine heavy chain immunoglobulin promoter
and encoding the leader signal peptide and 3' flanking sequence including a splice site
and intron sequences. The DNA fragments so produced for each Vh and Vk were
combined in a PCR using flanking primers required to obtain full-length DNA sequences.
The primer pairs used in these "linking" reactions were oligonucleotides OL411 / OL413
and OL414/OL415 for the Vh gene, whereas for the Vk gene, the oligonucleotides OL411
/ OL412 and OL411 / OL401 were used.

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The heavy chain gene complete with 5' and 3' flanking sequences was cloned into the expression vector pSVgpt [Reichmann et al (1988) *Nature*, 332: 323] which includes the human IgG1 constant region domain [Takahashi et al (1982) *Cell*, 29: 671] and the gpt gene for selection in mammalian cells. The light chain gene complete with 5' and 3'

5   flanking sequences was cloned into the expression vector pSVhyg [Reichmann et al *ibid*] in which the gpt gene is replaced by the gene for hygromycin resistance (hyg) and includes a human kappa constant region domain [Heiter et al (1980) *Cell*, 22: 197]. For both vectors, the fully assembled Vh or Vk genes were sub-cloned as HindIII / BamHI fragments purified by gel electrophoresis and handled using well known procedures and

10   reagent systems.

Table 2: Synthetic oligonucleotides for Vh

Name	Sequence	length
OL 373	GAAGTGAAGCTGGAGGAGTCTGGAGGCGGCTTGGTGCAAC	40
OL 374	CTGGAGGCTCCATGAAACTCTCCTGTGTTGCCTCTGGATT	40
OL 375	CATTTTCAGTAACCACTGGATGAACTGGGTCCGCCAGTCT	40
OL 376	CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGATCAA	40
OL 377	AATCGATTAATTCTGCAACACATTATGCGGAGTCTGTGAA	40
OL 378	AGGGAGGTTCACCATCTCAAGAGATGATTCCAAAAGTGCT	40
OL 379	GTGTACCTGCAAATGACCGACCTGAGAACTGAAGACACTG	40
OL 380	GCGTTTATTACTGTTCCAGGAATTACTACGGTAGTACCTA	40
OL 381	CGACTACTGGGGCCAAGGCACCACTCTCACAGTGTCCTCAGG	42
OL 382	CCTGAGGACACTGTGAGAGTGG	22
OL 383	TGCCTTGGCCCCAGTAGTCGTAGGTACTACCGTAGTAATT	40
OL 384	CCTGGAACAGTAATAAACGCCAGTGTCTTCAGTTCTCAGG	40
OL 385	TCGGTCATTTGCAGGTACACAGCACTTTTGGAATCATCTC	40
OL 386	TTGAGATGGTGAACCTCCCTTTCACAGACTCCGCATAATG	40
OL 387	TGTTGCAGAATTAATCGATTTTGATCTAATTTCAGCAACC	40
OL 388	CACTCAAGCCCCTTCTCTGGAGACTGGCGGACCCAGTTCA	40
OL 389	TCCAGTGGTTACTGAAAATGAATCCAGAGGCAACACAGGA	40
OL 390	GAGTTTCATGGAGCCTCCAGGTTGCACCAAGCCGCCTCCA	40
OL 391	GACTCCTCCAGCTTCACTTC	20
OL 413	AGACTCCTCCAGCTTCACTTCGGAGTGGACACCTGTGGAGAG	42
OL 414	ACCACTCTCACAGTGTCCTCAGGTGAGTCCTTACAACCTCTC	42
OL 415	TTGGGATCCTATAAATCTCTGGCC	24

Table 3: Synthetic oligonucleotides for Vk

Name	Sequence	length
OL 392	GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGA	40
OL 393	GTCCAGGAGAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCA	40
OL 394	GTTCGTTGGCTCAAGCATCCACTGGTATCAGCAAAGAACA	40
OL 395	AATGGTTCTCCAAGGCTTCTCATAAAGTATGCTTCTGAGT	40
OL 396	CTATGTCTGGCATCCCTTCTAGATTTAGTGGCAGTGGATC	40
OL 397	AGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT	40
OL 398	GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCT	40
OL 399	GGCCATTCACGTTCGGCTCGGGGACAAATTTGGAAGTAAA	40
OL 400	ACGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGGATCCTGGCAGAGTC	50
OL 401	GACTCTGCCAGGATCCAACTGAGGAAGCAA	30
OL 402	AGTTTAAATTCTACTCACGTTTTACTTCCAAATTTGTCCC	40
OL 403	CGAGCCGAACGTGAATGGCCAGCTATGACTTTGTTGACAG	40
OL 404	TAATAATCTGCAATATCTTCAGACTCCACAGTGTTGATGC	40
OL 405	TAAGAGTAAAATCTGTCCCTGATCCACTGCCACTAAATCT	40
OL 406	AGAAGGGATGCCAGACATAGACTCAGAAGCATACTTTATG	40
OL 407	AGAAGCCTTGGAGAACCATTTGTTCTTTGCTGATACCAGT	40
OL 408	GGATGCTTGAGCCAACGAACTGACTGGCCCTGCAGGAGAA	40
OL 409	ACTGACTCTTTCTCCTGGACTCACAGACAGGATGGCTGGA	40
OL 410	GACTGAGTCAGCAAGATGTC	20
OL 411	TTACGCCAAGCTTATGAATATGCAAATCC	29
OL 412	AGACTGAGTCAGCAAGATGTCGGAGTGGACACCTGTGGAGAG	42

EXAMPLE 4

Construction of modified antibody Vh and Vk genes.

A modified Vk gene termed Vk1 containing the mutations L3Q, A9D, I10T, L11S, V13A, I58V, S74T, T77S, V78L, S80A, I83A, D85T and L104V was constructed by gene synthesis. Table 4 lists the oligonucleotides listed used in the assembly of Vk1. These oligonucleotides were used, together with OL393, OL394, OL395, OL400, OL401, OL403, OL405, OL407 and OL408 (see example 3 above) in a gene synthesis reaction as previously. The gene was cloned into the pGEM-T easy vector (Promega) and several clones were sequenced until a correct clone was obtained. Assembly of the full-length immunoglobulin gene and sub-cloning to the expression vector was as per example 3 with

the exception that oligonucleotides OL411 and OL469 were used in the linking reaction for the Vk gene.

Additional mutations were introduced in the Vk gene to make further variant Vk genes. These mutations comprised: V19A, Q38H, R39T, S100G, N103K, V106I. The mutagenesis was conducted by PCR using the oligonucleotides listed in table 5. OL768 and OL769, OL770 and OL771 were used in overlap PCR, in combination with OL411 and OL401 (see above). OL648 was used in a single PCR in combination with OL411. The PCR products were cloned into pGEM-T Easy (Promega) and a correct clone identified by sequencing.

Variant Vh genes were also constructed from the wild-type sequence using mutagenesis. Variant Vh genes comprising the substitutions K3Q, E5V, M18L, K19R, V23A, I28T, I51T, I56T, E64D, S79N, A80S, V81L, T86N, D87S, R89K, G94A, T115L and L116V were constructed. These mutations were introduced using the oligonucleotides listed in table 6. Briefly, each set of oligonucleotides was used in overlap PCR, in combination with OL411 and OL415. The PCR products were cloned into pGEM-T Easy (Promega) and a correct clone identified by sequencing.

The Vh or Vk domains were sub-cloned into the expression vectors as HindIII BamHI fragments as previously and variant antibodies expressed according to the method detailed as example 5.

Table 4:   Synthetic oligonucleotides for Vk1 assembly

Name	Sequence	length
OL 459	GACATCCAGCTGACTCAGTCTCCAGACACCTCCTCTGCCA	40
OL 460	CTATGTCTGGCGTGCCTTCTAGATTTAGTGGCAGTGGATC	40
OL 461	AGGGACAGATTTTACTCTTACCATCAACTCCCTGGAGGCC	40
OL 462	GAAGATGCCGCAACCTATTACTGTCAACAAAGTCATAGCT	40
OL 463	GGCCATTCACGTTCGGCTCGGGGACAAATGTGGAAGTAAA	40
OL 464	AGTTTAAATTCTACTCACGTTTTACTTCCACATTTGTCCC	40
OL 465	TAATAGGTTGCGGCATCTTCGGCCTCCAGGGAGTTGATGG	40
OL 466	AGAAGGCACGCCAGACATAGACTCAGAAGCATACTTTATG	40
OL 467	ACTGACTCTTTCTCCTGGACTGGCAGAGGAGGTGTCTGGA	40
OL 468	GACTGAGTCAGCTGGATGTC	20
OL 469	AGACTGAGTCAGCTGGATGTCGGAGTGGACACCTGTGGAGAG	42

Table 5:   Synthetic oligonucleotides for Vk mutageneis

Name	Sequence	length
OL 648	GGATCCAACTGAGGAAGCAAAGTTTAAATTCTACTCACGTTTGATTTC CACCTTTGTCCCGCCGCCGAACGTGAATGGCC	80
OL 768	AGTCCAGGAGAAAGAGCCAGTTTCTCCTGCAGG	33
OL 769	CCTGCAGGAGAAACTGGCTCTTTCTCCTGGACT	33
OL 770	CCACTGGTATCAGCACACAACAAATGGTTCTCCAA	35
OL 771	TTGGAGAACCATTTGTTGTGTGCTGATACCAGTGG	35

Table 6:   Synthetic oligonucleotides for Vh mutagenesis

Name	Sequence	length
OL 642	GTCTCAGGGAGCCTCCAGGTTGCACCAAGCCGCCTCCAGACTCCACCAGC TGCACTTCGGAG	62
OL 643	AACCTGGAGGCTCCCTGAGACTCTCCTGTGCTGCCTCTGGATTCACTTTC AGTAACCACTGG	62
OL 644	AGGCTGTTCATTTGCAGGTACAGAGAATTTTTGGAATCATC	41
OL 645	TACCTGCAAATGAACAGCCTGAAAACTGAAGACACTGCCGTTTATTACTG	50
OL654	GAAACTAGATCAAAATCGACTAATTCTGCA	30
OL655	ATTAGTCGATTTTGATCTAGTTTCAGCAAC	30
OL656	CACATTATGCGGACTCTGTGAAAGGG	26
OL657	CCCTTTCACAGAGTCCGCATAATGTG	26
OL658	GGCCAAGGCACCCTTGTCACAGTGTCCTCA	30
OL659	TGAGGACACTGTGACAAGGGTGCCTTGGCC	30
OL899	GCCAAGGCACCACTGTCACAGTGTCCTCAGG	31
OL900	CCTGAGGACACTGTGACAGTGGTGCCTTGGC	31

5   **EXAMPLE 5**

Expression, purification and quantitation of anti-TNF alpha antibodies

The heavy and light chain expression vectors were co-transfected using electroporation into NS/0, a non-immunoglobulin producing mouse myeloma, obtained from the European Collection of Animal Cell Cultures (ECACC). Colonies expressing the gpt

10   gene were selected in Dulbecco's Modified Eagles Medium (DMEM) supplemented with 10% (v/v) foetal calf serum and antibiotics (all from Gibco, Paisley, UK) and with 0.8μg/ml mycophenolic acid and 250μg/ml xanthine (Sigma, Poole, UK).

Production of human antibody by transfected cell clones was measured by ELISA for

human IgG [Tempest et al (1991) *BioTechnology* 9: 266]. Cell lines secreting antibody

were expanded and antibody purified by protein A affinity chromatography [Harlow E.

Lane D.; in Antibodies a Laboratory Manual, pp 309; Cold Spring Harbor Laboratory

5   Press (1988), NY, USA].

The concentration of the purified antibody was determined using an ELISA detecting the

human kappa constant region of the antibodies of interest. A standard concentration

curve was determined for a commercial preparation of the therapeutic antibody infliximab

(Schering-Plough Ltd, UK) and the standard used to compute the concentration of the test

10   antibody preparation. The assay was conducted in 96-well plates and all determinations

were conducted in duplicate.

For the assay, plates (Dynatech Immulon 2) were coated using 100µl per well sheep anti-

human κ antibody (The Binding Site, Birmingham, UK) diluted 1:250 in

carbonate/bicarbonate coating buffer pH9.6 (Sigma, Poole, UK). Coating was conducted

15   for 1 hour at 37°C and the wells washed 3 times with PBST (PBS with 0.05% Tween 20).

The wells were filled with 100 µL of PBST and the dilutions for the control and test

antibodies set out. The negative control uses PBST only and no antibody was added. The

standard preparation (infliximab) was diluted 1:1000 (v/v) and a doubling dilution series

set out across the plate. Doubling dilution series were also set out for the test antibody

20   preparations. The plate was incubated at room temperature for 1 hour and the wells

washed as previously. Bound antibody was detected using a peroxidase conjugated sheep

ant-human IgG γ chain specific reagent (The Binding Site, Birmingham, UK). This

secondary antibody was diluted 1:1000 in PBST and 100 µl added to each well of the

plate. The plate was incubated for a further 1 hour at room temperature and washed as

25   previously. Detection was achieved using 100ul per well "Sigmafast" peroxidase

substrate (Sigma, Poole, UK) and the colour development stopped by addition of 40ul per

well 1M sulphuric acid. The optical density was read using a plate reader at 492nm. A

standard curve of antibody concentration versus A_{492} was plotted for the control antibody

and the concentration of the test antibody determined by comparison with the standard.

30

EXAMPLE 6

Protection of TNF alpha sensitive cells in vitro by TNF alpha neutralisation using
modified antibodies

The ability of anti-TNF alpha antibodies to neutralise the lethal effect of TNF alpha on a cell line grown *in vitro* was tested using the scheme provided by Galloway [Galloway *et al.* 1991 *J. Immunol. Meth.* 140:37-43]. The assay uses the murine fibrosarcoma cell line WEHI164, a line which is very sensitive to the lethal effect of TNF alpha.

5   For the assay, cells were grown overnight in the presence of a fixed, lethal concentration of TNF alpha and a range of different antibody concentrations. The next day, the metabolic activity of cells was measured as an indication of survival. Antibodies that neutralise TNF alpha confer a protective effect to the cells and thereby a greater metabolic activity is measured in the assay.

10   WEHI164 were obtained from the European Collection of Animal Cell Cultures (ECACC #. 8702250) and grown in DMEM medium with Glutamax, (Gibco, Paisley, UK), 10% foetal calf serum (Perbio, Chester, UK) and containing antibiotic-mycotic (Gibco). On the day prior to assay, cells are sub-cultured to ensure active proliferation during the subsequent assay period. The assay was conducted in 96 well plates in duplicate for all

15   treatments. Plates were prepared to contain dilutions of control antibody, test antibody and negative control with no antibody. Typically, doubling dilution series of the antibodies were arranged across a plate starting from a concentration of $10\mu g/ml$ antibody in a volume of $50\mu l$. A stock solution of TNF alpha (PeproTech EC Ltd, London, UK) at $50\mu g/ml$ in medium containing $4\mu g/ml$ of actinomycin was prepared and added to the

20   treatment wells. The TNF alpha solution was mixed by gently tapping the plate and the plate incubated for at least two hours at room temperature before the prepared solutions were transferred to the assay plate containing the cells.
The assay plate was prepared by seeding 2.5×10^4 cells in $50\mu l$ per well and incubating for at least 1hour at 37°C, 5% CO_2. Following this, $50\mu l$ of the TNF alpha/antibody mixture

25   or control preparation was transferred from the plate used to dilute out the various treatments. The cell and treatment mixtures were mixed by gently tapping the plate and the plate incubated overnight at 37°C in a humidified atmosphere containing 5% CO_2. Next day, the metabolic activity of the cells in each well was assessed using a "CellTiter 96 Aqueous One Solution Cell Proliferation Assay" (Promega, Southampton, UK).

30   Following addition of the assay solution, the plates were incubated for a further 90 minutes and the absorbance of the solutions in each well was read using a plate reader at 492nm. The absorbance figures are plotted versus antibody concentration. In all assays the positive control preparation was a sample of the therapeutic antibody infliximab

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(Schering-Plough Ltd, UK), which in this assay consistently demonstrates significant TNF alpha neutralisation at concentrations of less than $0.1\mu g/ml$. Similarly the modified antibody of the present invention consistently demonstrated a protective effect in this assay equivalent to the positive control preparation. FIGURE 2 shows an example plot

5 from this assay.

EXAMPLE 7

Neutralisation of TNF alpha stimulated production of ICAM-1 by human endothelial cells in vitro.

10 The ability of anti-TNF alpha antibodies to neutralise TNF alpha stimulated production in human umbilical vein endothelial (HUVE) cells of membrane bound ICAM-1, was tested in an *in vitro* assay. Briefly, HUVE cells are grown in a 96-well plate in the presence of TNF alpha and varying concentrations of test or control antibody. The quantitative relative expression of membrane bound ICAM-1 is subsequently assessed by cell lysis

15 and an enzyme linked immunoabsorbance assay (ELISA) using a commercially available ICAM-1 detection system.

For the assay, two parallel sets of 96 well plates are prepared. One set, termed the "assay plate", is seeded with cells, the other, termed the "preparation plate", is used to prepare the dilutions of TNF alpha and the test and control antibody solutions. The contents of

20 the preparation plate are ultimately transferred to the assay plate. All assays are conducted in duplicate.

For the assay plate, HUVE cells (Cambrex Bio Science, Wokingham, UK) were seeded at a density of 5×10^4 cells per well in a volume of $50\mu l$. The cells were allowed to adhere to the plate by incubation at $37^{\circ}C$, 5% CO_2 for at least 2 hours.

25 For the preparation plate, doubling dilution series of the test and positive control antibody were set out in duplicate across the plate. The starting concentration for the antibodies was $20\mu g/ml$ in a final volume of $100\mu l/well$. The negative control received no antibody. A solution of 40ng/ml TNF alpha (PeproTech EC Ltd, London, UK) in medium was prepared and $100\mu l$ per well added to each of the treatment wells on the preparation plate.

30 The plate was mixed by gentle tapping and incubated for 45 minutes at room temperature. Following this incubation, $50\mu l$ from each well of the preparation plate was added to its corresponding well in the assay plate. The assay plate was incubated for 23 hours at $37^{\circ}C$ in a humidified atmosphere containing 5% CO_2.

Next day, the medium from all wells was removed and the cells washed once with
phosphate buffered saline (PBS). The cells were lysed and the lysate assayed for the
presence of ICAM-1. Lysis was achieved by incubation at 4°C for 45 minutes in 80μl
lysis buffer. Lysis buffer comprised 8.7g/l NaCl, 6.05g/l Tris 0.5%(v/v) NP40, at pH to

5   8.0. Lysis buffer also contained protease inhibitors PMSF, iodoacetamide and benzamide
at 100mM concentration and pepsatin A and leupeptin at 50mM and 5mM concentrations
respectively. These inhibitors were added fresh to the lysis buffer preparation at time of
use.

The well contents were mixed using a micropipette before removing the lysate to a fresh

10   round-bottom 96 well plate. The plate was spun to clear precipitated cell debris and the
cleared lysate removed to a further fresh 96 well plate for storage, (-20°C) or immediate
assay.

For assay, 20μl of cleared lysate was analyzed for the presence of solubilized ICAM-1
using a commercial ELISA system (sICAM-1 Module set; Bender Medsystems,

15   Towcester, UK) and conditions recommended by the supplier. The absorbance of the
solutions in each well was read using a plate reader at 492nm. The absorbance figures
were plotted versus antibody concentration. In all assays the positive control preparation
was a sample of the therapeutic antibody infliximab (Schering-Plough ltd), which in this
assay consistently demonstrates significant TNF alpha neutralisation at concentrations of

20   less than 1μg/ml. Similarly the modified antibody of the present invention consistently
demonstrates a concentration dependent inhibition ICAM-1 expression equivalent to the
positive control preparation. FIGURE 3 shows an example plot from this assay.

EXAMPLE 8

25   *Competition assay of modified antibodies for binding to TNF alpha*
The ability of the modified antibodies of the present invention to compete with the TNF
alpha receptor (RII, p75) is measured in a competition ELISA, based on Siegel *et al*
[Siegel *et al.* (1995) *Cytokine* 7(1):15-25]. ELISA plates were coated with the receptor
(TNF alpha RII-Fc) and incubated with a mixture of a fixed amount of biotinylated TNF

30   alpha and a doubling dilution series of the antibody. Binding of TNF alpha to the
receptor was measured by colourimetric assay using a Streptavidin-HRP conjugate.
The assay was conducted using Immulon 2HB 96 well plates, (Fisher, Loughborough,
UK) prepared by coating overnight at 4°C with 5μg/ml TNF alpha RII-Fc (R&D Systems,

Abingdon, UK) in carbonate coating buffer. A volume 50μl was applied to each well of the plate. The coated plates were washed at least five times with PBS-0.05% (v/v)Tween 20, (PBS-T) and blocked by addition of a solution of 1% (v/v) BSA in PBS-T and further incubation at room temperature for at least one hour.

5   During this incubation, a dilution plate was set up in which the test antibody and control reagents were set out. Typically a doubling dilution series starting at a concentration of 50μg/ml in a final volume of 50μl/well was used for each test antibody. Controls included non-TNF alpha binding antibody as a negative, and a preparation of clinical grade Infliximab (Schering-Plough ltd, UK) as the positive. Control antibodies were of

10   the same isotype as the test antibodies. Following addition of the antibodies, 50μl per well of a solution of 50ng/ml biotin-TNF alpha was added and the plate mixed by gentle tapping. The TNF alpha was a commercially sourced product as previously (Peprotech, London, UK) and biotinylated using EZ link Sulfo-NHS-biotin (Perbio,Tattenhall, UK) and the suppliers recommended protocol.

15   The blocking solution was removed from the assay plate and the plate washed as previously. 50μl from each well of the dilution plate was added to the relevant well of the assay plate and following mixing, the assay plate incubated for at least one hour at room temperature. Following incubation, the plate was washed and 100μl of a diluted Streptavidin-HRP (Sigma, Poole, UK) reagent added to all wells of the plate. The plate

20   was further incubated for at least one hour at room temperature and washed as previously. The assay is disclosed using Sigma-fast OPD tablets (Sigma, Poole, UK), 100μl/well and the colour reaction stopped by adding 50μl per well 1M Sulphuric acid. The plate was read and the results plotted as antibody concentration versus absorbance at 492nm. FIGURE 4 shows an example plot from this assay. The preferred antibody of the present

25   invention shows a concentration dependent competition curve for TNF alpha binding equivalent to that for the positive control antibody in this assay.

EXAMPLE 9

Inhibition of TNF alpha induced up-regulation of IL-6 in Hs 27 cells

30   Human foreskin fibroblast cells can be induced to produce IL-6 by exposure to TNF alpha. The ability of the modified antibodies of the present invention to block this up-regulation of expression was assessed by co-incubation of the cells with TNF alpha and

the test antibodies, followed by a determination of the subsequent IL-6 levels secreted into the medium using a commercially available IL-6 detection system.

For the assay, two parallel sets of 96 well plates are prepared. One set, termed the "assay plate", is seeded with cells, the other, termed the "preparation plate", is used to prepare

5   the dilutions of TNF alpha and the test and control antibody solutions. The contents of the preparation plate are ultimately transferred to the assay plate. All assays are conducted in duplicate.

For the assay plate, human foreskin fibroblast cells Hs 27, obtained from the European Collection of Animal Cell Cultures (ECACC no. 94041901), were seeded at a density of

10   $2x10^4$ cells per well and the cells allowed to adhere to the plate by overnight incubation at 37°C in a humidified atmosphere containing 5% CO_2. The culture medium throughout was DMEM + Glutamax (Gibco, Paisley, UK) containing 10% foetal calf serum (Perbio, Chester, UK) and a conventional antibiotic/mycotic preparation (Gibco).

For the preparation plate, doubling dilution series of the test and positive control antibody

15   were set out in duplicate across the plate. The starting concentration for the antibodies was 1.25µg/ml in a final volume of 100µl/well. The negative control received no antibody. A solution of 3ng/ml TNF alpha (PeproTech EC Ltd., London) was added to all antibody-containing wells, for the control wells with no antibody, an additional 100µl/well of medium is added. The plate was mixed by gentle tapping and incubated at

20   room temperature for at least 30 minutes.

Medium was removed from the assay plate containing the Hs 27 cells and 100µl from each well of the preparation plate was transferred to the relevant well of the assay plate. The plate was mixed by gentle tapping and incubated for at least 18 hours at 37°C in a humidified atmosphere containing 5% CO_2. Following incubation, the medium was

25   removed from each well to a fresh U-bottomed 96 well plate for storage at –20°C or immediate assay.

The medium was analysed for the presence of IL-6 using a commercial ELISA system (IL-6 Module set; Bender Medsystems, Towcester, UK) and conditions recommended by the supplier. For assay, 50µl of medium was diluted 1:15 (v/v). The absorbance of the

30   solutions in each well was read using a plate reader at 492nm. The absorbance figures were plotted versus antibody concentration. In all assays the positive control preparation was a sample of the therapeutic antibody infliximab (Schering-Plough ltd, UK). The preferred modified antibody of the present invention consistently demonstrates a

concentration dependent inhibition IL-6 expression. FIGURE 9 shows an example plot from this assay.

EXAMPLE 10

5   *Detection of TNF alpha*

A simple plate ELISA was used to confirm the ability of the modified antibody of the present invention to bind TNF alpha. The assay was conducted in comparison with a preparation of the therapeutic antibody Infliximab (Schering-Plough ltd, UK) as positive control and a non-TNF alpha binding human IgG preparation (Sigma I2511) as a negative

10   control. The assay was conducted using the method detailed below and demonstrates that the preferred composition (Vh5/Vk12) of the present invention has equal efficacy to the control antibody in this assay. A typical binding curve is depicted as FIGURE 7. Immulon 2HB 96 well plates, (Fisher, Loughborough, UK) were coated overnight at 4°C with 2.5μg/ml TNF alpha (Peprotech, London, UK) in carbonate coating buffer. A

15   volume of 50μl was applied to each well of the plate. The coated plates were washed three times with PBS-0.05% (v/v)Tween 20, (PBS-T).

A doubling dilution series of each antibody was prepared and applied in a volume of 100μl per well, each in duplicate. The highest antibody concentration was 1μg/ml. Plates were incubated for 1 hour at room temperature and washed as previously with PBST. To

20   detect bound antibody, plates were incubated with a Mouse-anti human IgG-HRP conjugate (Sigma, Poole, UK) preparation diluted 1/1000 in PBST. Incubation was for at least 90 minutes at room temperature. The plates were again washed as previously using PBST and the bound antibody disclosed using 100μl/well of Sigma-Fast OPD. The color was allowed to develop for 5 minutes and the reaction stopped by addition of 40 μl/well

25   of 1M H_2SO_4. The plates were read at 492nm and the data plotted as concentration of antibody versus the optical density. FIGURE 7 shows a representative binding curve indicating functional equivalence in this assay between the modified antibody (Vh5/Vk12) and the positive control.

30   **EXAMPLE 11**

Demonstration of reduced immunogenic potential in modified anti-TNF alpha antibody using human PBMC in vitro proliferation assay.

The modified antibody was prepared according to the method of example 5. Positive control (challenge antibody) was clinical grade infliximab (Schering-Plough ltd, UK). For T cell proliferation assays 4×10^6 PBMC (per well) from healthy donors were incubated with unmodified and modified antibodies in 2ml bulk cultures (in 24 well

5   plates). Each donor was treated with modified and unmodified antibodies at 5 and 50μg/ml. In addition an untreated control bulk culture was maintained enabling stimulation indexes to be determined. At days 5, 6, 7 and 8 cells for each bulk culture were gently agitated and 50μl samples removed in triplicate for determination of the proliferation index. The 50μl sample aliquots were each transferred to 3 wells of a U-

10   bottom 96 well plate. Fresh AIM V media (130□l) was added to each of the 96 wells. Cells were pulsed (for 18-21 hours) with 1μCi [^{3}H]Thymidine per well diluted in a total volume of 20ul AIM V media. The total volume for each culture was 200μl. CPM values were collected using a beta-plate reader and the stimulation index for each time point determined as per example 2 above.

15   The SI was plotted for each time point and antibody treatment. A significant SI was taken as >2.0. In responsive donors, treatment with infliximab results in a significant proliferative response with a peak at day 7. In the same donors, treatment with the modified antibody composition (Vh5/Vk12) of the present invention does not result in a significant proliferative response. This result indicates a reduced immunogenic potential

20   in the preferred antibody composition of the present compared with the parental antibody. A representative plot from this assay is provided in FIGURE 10.

PATENT CLAIMS

1. A modified monoclonal anti-TNF alpha antibody being substantially non-immunogenic or less immunogenic than any non-modified antibody having essentially the same biological specificity when used in vivo, and comprising specific amino acid residues having alterations in the V- region of its heavy and / or light chain compared with the non-modified parental antibody, wherein said alterations cause a reduction or an elimination of the number of peptide sequences within said V-region, which act in the parental antibody as MHC class II binding ligands and stimulate T-cells,.

2. A modified antibody according to claim 1, wherein the parental antibody is chimeric A2 (cA2).

3. A modified antibody according to claim 1 or 2, wherein the alterations in the V – region additionally were conducted in the CDRs of the antibody essentially retaining the binding affinity of the parental antibody.

4. A modified antibody according to claim 2 or 3, wherein said peptide sequences to be altered within said V-region of the non-modified antibody are selected from the group of contiguous T-cell epitope sequences as depicted in Figure 1 and Table 1.

5. A modified antibody according to claim 4, wherein 1- 9 amino acids are altered in any of said T-cell epitopes.

6. A modified antibody according to claim 5, wherein 1 amino acid is altered.

7. A modified antibody according to claim 5 or 6, wherein said alteration of amino acid residues is achieved by substitution.

8. A modified antibody according to any of the claims 4 to 7, wherein further amino acid residue alterations are conducted to restore biological activity of said antibody.

9. A modified antibody according to any of the claims 3 to 8, wherein said amino acid residue alterations in the V – region are conducted in at least one of the peptide strings of contiguous amino acid residues of the parental antibody, selected from the group consisting of:

(A)	GLVQPGGSMKLSCVAS;
(B)	WVAEIRSKSINSA;
(C)	SRDDSKSAVYLQMTDLRT;
(D)	RNYYGSTYDYWGQGTTLTVSS;
(E)	DILLTQSPAILSVSPGERVSF;
(F)	HWYQQRTNGSPR;
(G)	LIKYASESMSGIPS;
(H)	DFTLSINTVESEDIADYYCQQ.

10. A modified antibody according to claim 2 or 3, wherein the V – region heavy chain ("Vh" chain) comprises a sequence selected from the group consisting of SEQ ID 1 (Vh1), SEQ ID 2 (Vh3), SEQ ID 3 (Vh5) and SEQ ID 4 (Vh8).

11. A modified antibody according to claim 2 or 3, wherein the V – region light chain ("Vk" chain) comprises a sequence selected from the group consisting of SEQ ID 5 (Vk1), SEQ ID 6 (Vk12), SEQ ID 7 (Vk5) and SEQ ID 8 (Vk8).

12. A modified antibody according to claim 10 or 11, comprising any of the Vh chains of claim 10 and any of the Vk chains of claim 11.

13. A modified antibody of claim 12, comprising Vh5 chain (SEQ ID 3) and Vk12 chain (SEQ ID 6).

14. A modified antibody of claim 12, comprising Vh1 chain (SEQ ID 1) and Vk1 chain (SEQ ID 5).

15. A modified antibody of claim 12, comprising Vh1 chain (SEQ ID 1) and Vk5 chain (SEQ ID 7).

16. A modified antibody of claim 12, comprising Vh1 chain (SEQ ID 1) and Vk8 chain (SEQ ID 8).

17. A modified antibody of claim 12, comprising Vh8 chain (SEQ ID 4) and Vk5 chain (SEQ ID 7).

18. A modified antibody of claim 2 or 3 having an altered V- region heavy chain, comprising any of the following groups of substitutions of amino acid residues compared with the non-altered cA2 antibody:

(a1)   M18L, K19R, V23A, I28T, I51T, I56T, S79N, A80S, V81L, T86N, D87S, R89K, L116V;

(a2)   K3Q, E5V, M18L, K19R, V23A, I28T, S79N, A80S, V81L, T86N, D87S, R89K, G94A;

(a3)   M18L, K19R, V23A, I28T, S79N, A80S, V81L, T86N, D87S, R89K, L116V;

(a4)   K3Q, E5V, M18L, K19R, V23A, I28T, I51T, I56T, E64D, S79N, A80S, V81L, T86N, D87S, R89K, G94A, T115L, L116V.

19. A modified antibody of claim 2 or 3 having an altered V- region light chain, comprising any of the following groups of substitutions of amino acid residues compared with the non-altered cA2 antibody:

(b1)   L3Q, A9D, I10T, L11S, V13A, V19A, Q38H, R39T, I58V, S74T, T77S, V78L, S80A, I83A, D85T;

(b2)   L3Q, A9D, I10T, L11S, V13A, I58V, S74T, T77S, V78L, S80A, I83A, D85T, L104V;

(b3)   L3Q, A9D, I10T, L11S, V13A, I58V, S74T, T77S, V78L, S80A, I83A, D85T, S100G, N103K, L104V, V106I;

(b4)   L3Q, A9D, I10T, L11S, V13A, V19A, Q38H, R39T, I58V, S74T, T77S, V78L, S80A, I83A, D85T, S100G, N103K, L104V, V106I.

20. A modified antibody of claim 2 or 3 having altered V- region heavy and light chains comprising simultaneously any of the groups of amino acid substitutions a1 – a4 as indicated in claim 18 and any of the groups of amino acid substitutions b1 – b4 as indicated in claim 19.

21. A modified antibody of claim 20 having altered V- region heavy and light chains comprising simultaneously the groups of substitutions a1 and b1.

22. A modified antibody of claim 20 having altered V- region heavy and light chains comprising simultaneously the groups of substitutions a2 and b2.

23. A modified antibody of claim 20 having altered V- region heavy and light chains comprising simultaneously the groups of substitutions a2 and b3.

24. A modified antibody of claim 20 having altered V- region heavy and light chains comprising simultaneously the groups of substitutions a2 and b4.

25. A modified antibody of claim 20 having altered V- region heavy and light chains comprising simultaneously the groups of substitutions a4 and b3.

26. A modified antibody according to any of the claims 1 – 25, wherein the constant region domains derive from human IgG1 and human kappa.

27. A modified antibody according to any of the claims 1 to 26, wherein when tested as a whole protein in a biological assay of induced cellular proliferation of human T-cells exhibits a stimulation index smaller than the parental antibody tested in parallel using cells from the same donor wherein said index is taken as the value of cellular proliferation scored following stimulation by the protein and divided by the value of cellular proliferation scored in control cells not in receipt of protein and wherein cellular proliferation is measured by any suitable means.

28. A modified antibody according to any of the claims 1 to 26, comprising V-region sequences from which peptides can be derived and tested in a biological assay of induced cellular proliferation of human T-cells and exhibit a stimulation index smaller than the stimulation index scored by peptides derived from the non-modified parental antibody and tested in parallel wherein said index is taken as the value of cellular proliferation scored following stimulation by the peptide and divided by the value of

cellular proliferation scored in control cells not in receipt of peptide and wherein cellular proliferation is measured by any suitable means.

29. A DNA molecule coding for an antibody according to any of the claims 1 to 28.

30. A pharmaceutical composition comprising a modified anti-TNF alpha antibody as defined in any of the above-cited claims, optionally together with a pharmaceutically acceptable carrier, diluent or excipient.

31. Use of an altered anti-TNF alpha antibody as defined in any of the above-cited claims for the manufacture of medicament for the treatment of rheumatoid arthritis and Crohn's disease.

32. A peptide molecule consisting of 9 – 15 consecutive amino acid residues, having a potential MHC class II binding activity and created from the primary sequence of non-modified anti-TNF alpha antibody A2, whereby said peptide molecule has a stimulation index of at least 1.8 to 2 in a biological assay of cellular proliferation wherein said index is taken as the value of cellular proliferation scored following stimulation by a peptide and divided by the value of cellular proliferation scored in control cells not in receipt peptide and wherein cellular proliferation is measured by any suitable means.

33. A peptide molecule of claim 32 selected from the group of contiguous T-cell epitope sequences as depicted in Figure 1 or Table 1.

34. A peptide molecule modified from the peptide molecule of claim 32 or 33 by amino acid substitution, having a reduced or absent potential MHC class II binding activity expressed by a stimulation index of less than 2, whereby said index is taken as the value of cellular proliferation scored following stimulation by a peptide and divided by the value of cellular proliferation scored in control cells not in receipt peptide and wherein cellular proliferation is measured by any suitable means.

35. A modified peptide molecule according to claim 34, having a stimulation index of less than 1.8.

36. Use of a peptide according to any of the claims 32 to 35 for the manufacture of an anti-TNF alpha antibody having substantially no or less immunogenicity than any non-modified parental antibody when used *in vivo*.

FIGURE 1

FIG1A

Peptide sequences from heavy chain variable region of anti-
TNFα antibody A2 with potential human MHC class II binding
activity.

VKLEESGGGLVQP,	GGLVQPGGSMKLS,	GLVQPGGSMKLSC,
GSMKLSCVASGFI,	MKLSCVASGFIFS,	SCVASGFIFSNHW,
SGFIFSNHWMNWV,	GFIFSNHWMNWVR,	FIFSNHWMNWVRQ,
NHWMNWVRQSPEK,	HWMNWVRQSPEKG,	MNWVRQSPEKGLE,
NWVRQSPEKGLEW,	KGLEWVAEIRSKS,	LEWVAEIRSKSIN,
EWVAEIRSKSINS,	AEIRSKSINSATH,	KSINSATHYAESV,
THYAESVKGRFTI,	ESVKGRFTISRDD,	GRFTISRDDSKSA,
FTISRDDSKSAVY,	SAVYLQMTDLRTE,	AVYLQMTDLRTED,
VYLQMTDLRTEDT,	LQMTDLRTEDTGV,	TDLRTEDTGVYYC,
TGVYYCSRNYYGS,	GVYYCSRNYYGST,	VYYCSRNYYGSTY,
RNYYGSTYDYWGQ,	NYYGSTYDYWGQG,	STYDYWGQGTTLT,
YDYWGQGTTLTVS		

FIG1B

Peptide sequences from light chain variable region of anti-
TNFα antibody A2 with potential human MHC class II binding
activity.

DILLTQSPAILSV,	ILLTQSPAILSVS,	PAILSVSPGERVS,
AILSVSPGERVSF,	LSVSPGERVSFSC,	ERVSFSCRASQFV,
VSFSCRASQFVGS,	SQFVGSSIHWYQQ,	QFVGSSIHWYQQR,
SSIHWYQQRTNGS,	IHWYQQRTNGSPR,	HWYQQRTNGSPRL,
PRLLIKYASESMS,	RLLIKYASESMSG,	LLIKYASESMSGI,
IKYASESMSGIPS,	ESMSGIPSRFSGS,	SGIPSRFSGSGSG,
SRFSGSGSGTDFT,	TDFTLSINTVESE,	FTLSINTVESEDI,
LSINTVESEDIAD,	NTVESEDIADYYC,	EDIADYYCQQSHS,
ADYYCQQSHSWPF,	DYYCQQSHSWPFT,	HSWPFTFGSGTNL,
WPFTFGSGTNLEV		

Peptides are 13mers, amino acid are identified using single
letter codes.

FIGURE 2

Neutralisation of the TNFα induced killing of WEHI164 cells
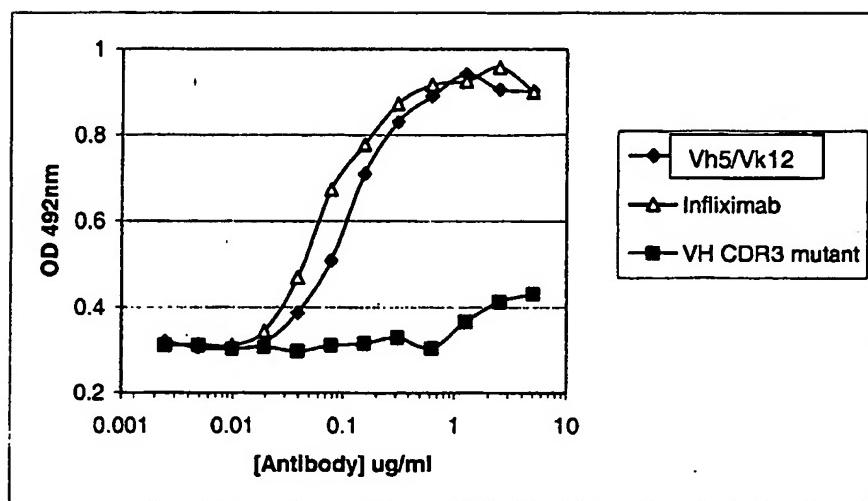
FIGURE 3

Neutralisation of the TNFα stimulated production of ICAM-1 in HUVE cells
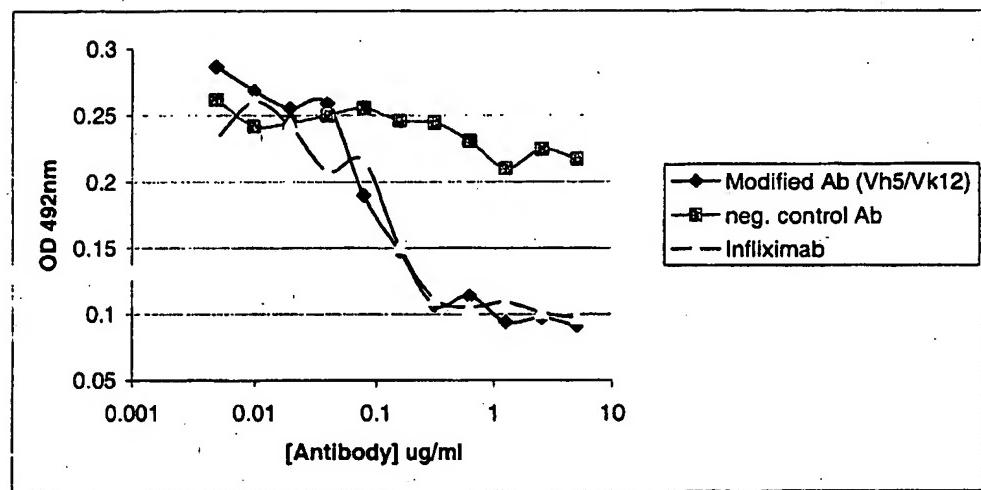
FIGURE 4

Competition with TNF-receptor for binding TNFα

FIGURE 5

Donor 4: peptides CA1-CA16

Donor 4: peptides CA17-CA32

Donor 4: peptides CA33-CA48

Donor 4: peptides CA49-CA64

Donor 4: peptidesCA65-CA75 + contols
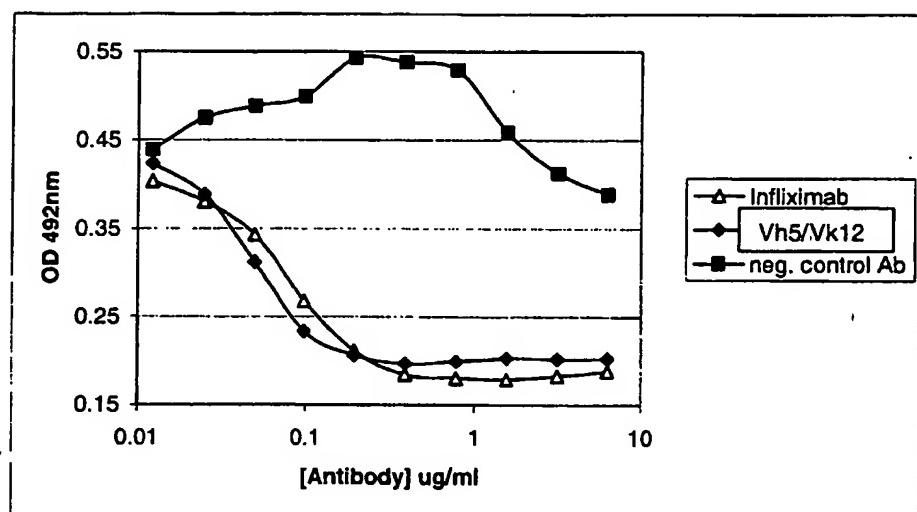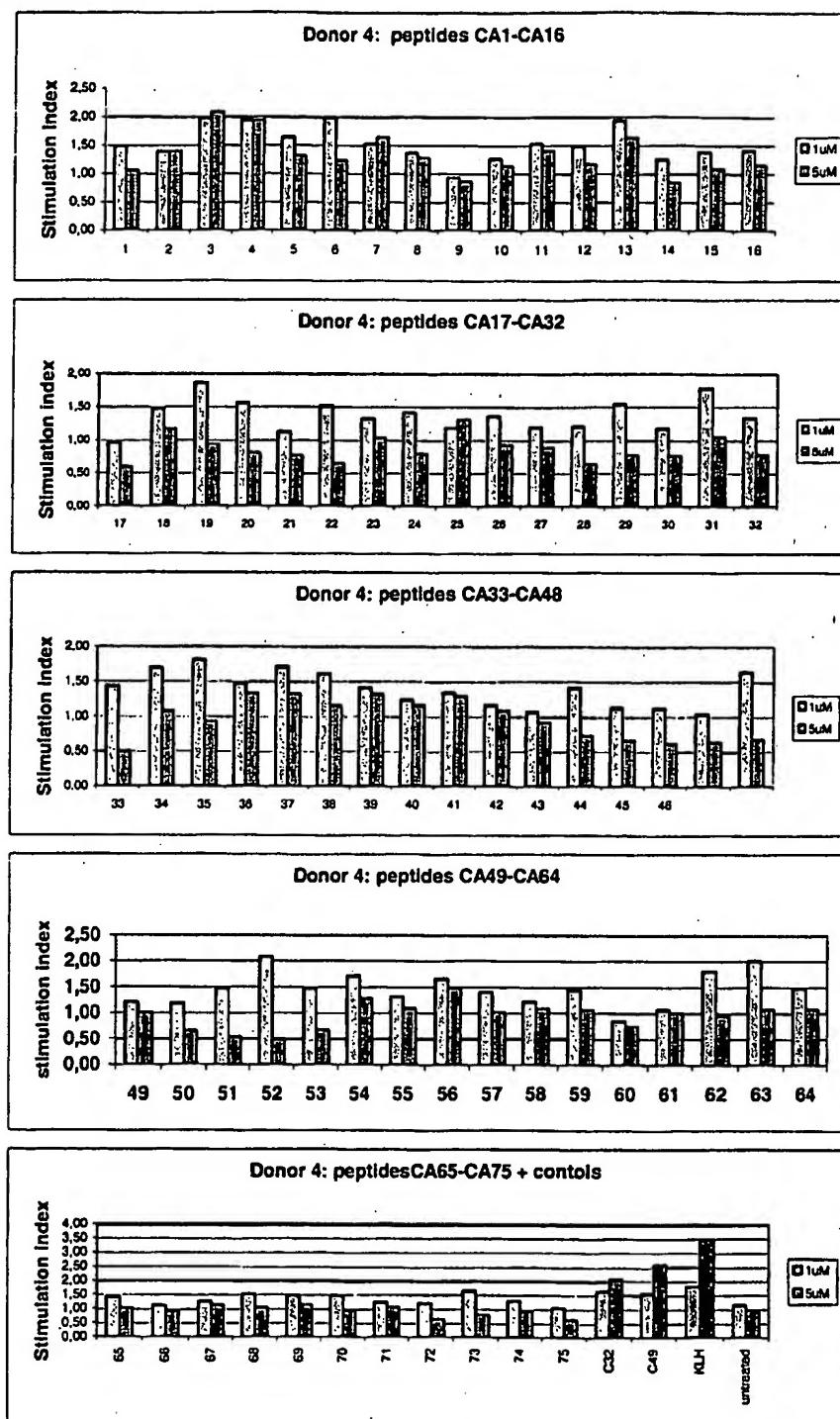
FIGURE 6

A) Donor #2 response to stimulation with peptides P1-P15
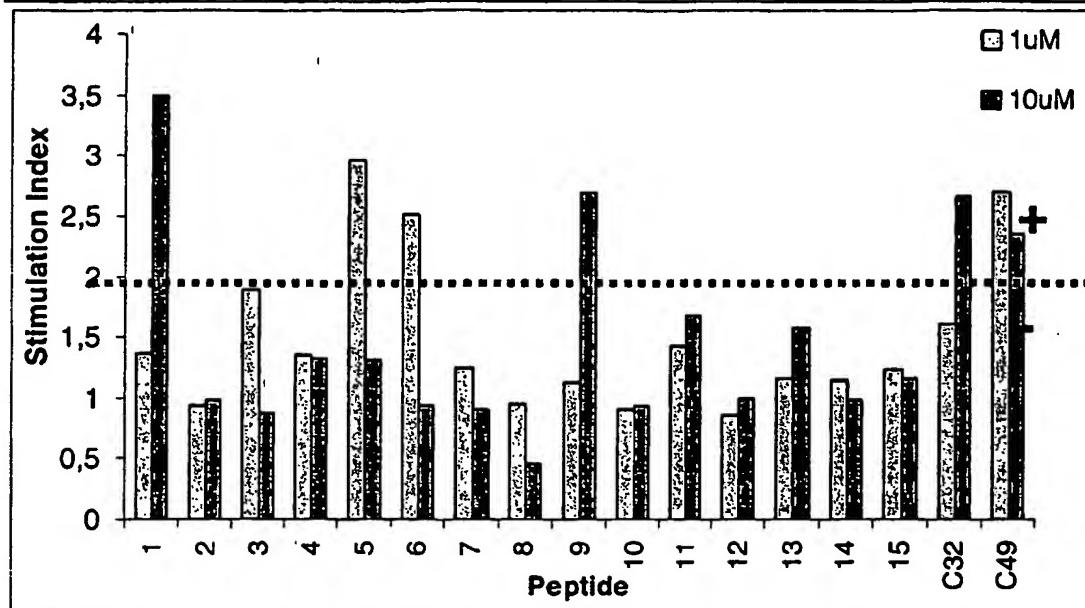
B) Donor #4 response to stimulation with peptides P1-P15

FIGURE 7

Detection of TNFα
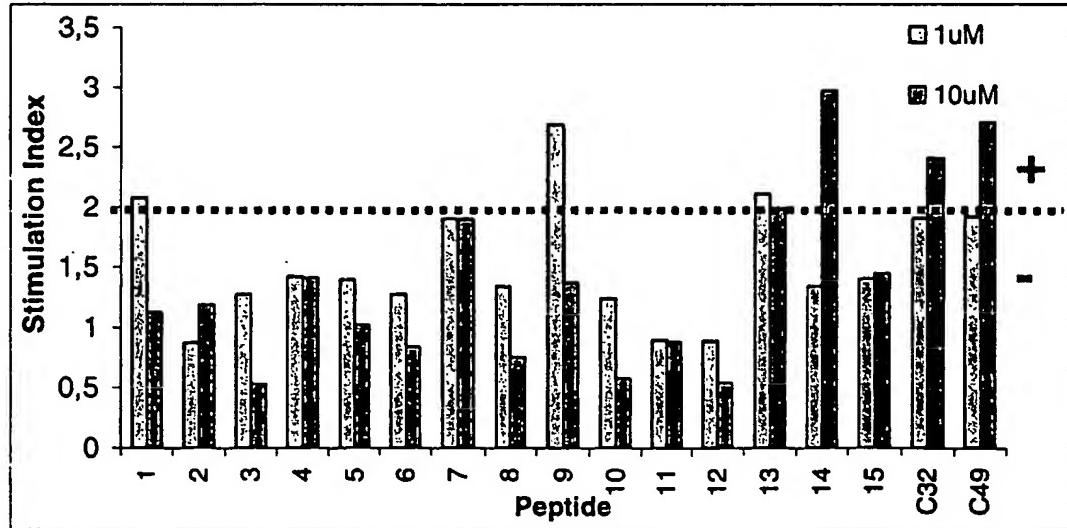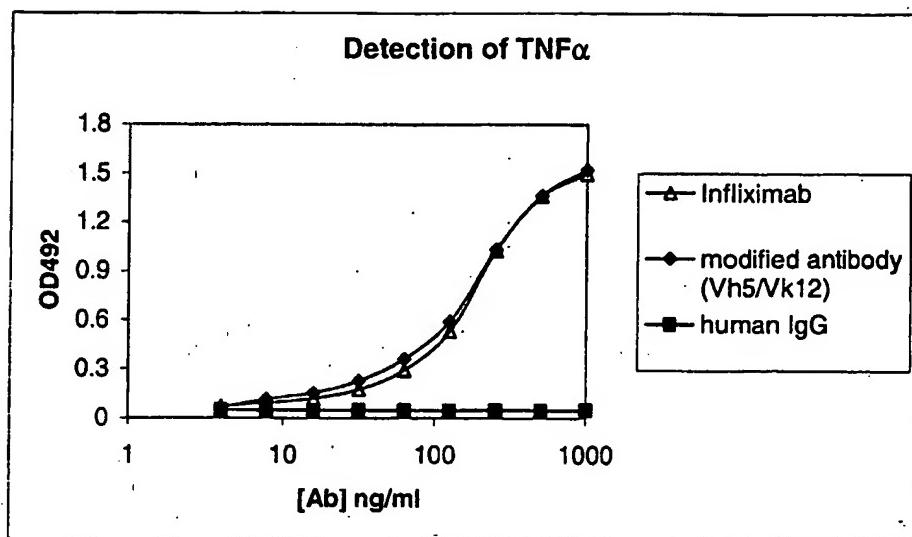
FIGURE 8

Vh1   (SEQ ID 1)
      EVQLVESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAEIRSKS
      INSATHYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCSRNYYGSTYDYW
      GQGTTLTVSS

Vh3   (SEQ ID 2)
      EVKLEESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAEIRSKS
      INSATHYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTGVYYCSRNYYGSTYDYW
      GQGTTVTVSS

Vh5   (SEQ ID 3)
      EVKLEESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAETRSKS
      TNSATHYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTGVYYCSRNYYGSTYDYW
      GQGTTVTVSS

Vh8   (SEQ ID 4)
      EVQLVESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQSPEKGLEWVAETRSKS
      TNSATHYADSVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCSRNYYGSTYDYW
      GQGTLVTVSS

Vk1   (SEQ ID 5)
      DIQLTQSPDTSSASPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESM
      SGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGSGTNVEVKR

Vk12 (SEQ ID 6)
      DIQLTQSPDTSSASPGERASFSCRASQFVGSSIHWYQHTTNGSPRLLIKYASESM
      SGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGSGTNLEVKR

Vk5   (SEQ ID 7)
      DIQLTQSPDTSSASPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESM
      SGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGGGTKVEIKR

Vk8   (SEQ ID 8)
      DIQLTQSPDTSSASPGERASFSCRASQFVGSSIHWYQHTTNGSPRLLIKYASESM
      SGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSHSWPFTFGGGTKVEIKR

FIGURE 9

IL-6 Expression in HS 27 Fibroblasts

FIGURE 10

A: responsive donor

Legend:
—△— Vh5/Vk1 2 5ug/ml
—▲— Vh5/Vk1 2 50ug/ml
—■— Infliximab 5ug/ml
—□— Infliximab 50ug/ml

B: non-responsive donor

(54) Title: MODIFIED ANTI-TNF ALPHA ANTIBODY

(57) Abstract: The invention relates to the modification of antibodies reactive to human tumor necrosis factor alpha (TNF alpha) to result in anti-TNF alpha antibodies that are substantially non-immunogenic or less immunogenic than any non-modified parental antibody when used in vivo. The invention relates also to peptide molecules comprising T-cell epitopes of the V-regions of the parental antibody which are modified by amino acid alteration in order to reduce or eliminate said T-cell epitopes.

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7   C07K16/24   C07K16/46   C12N15/13   A61K39/395   C07K7/04

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7   C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the International search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, EMBASE, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 92 16553 A (UNIV NEW YORK ;CENTOCOR INC (US)) 1 October 1992 (1992-10-01) page 10; examples 18-28	2-31, 33-36
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-/--

[X] Further documents are listed in the continuation of box C.   [X] Patent family members are listed in annex.

° Special categories of cited documents :

'A' document defining the general state of the art which is not considered to be of particular relevance

'E' earlier document but published on or after the International filing date

'L' document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

'O' document referring to an oral disclosure, use, exhibition or other means

'P' document published prior to the International filing date but later than the priority date claimed

'T' later document published after the International filing date or priority date and not In conflict with the application but cited to understand the principle or theory underlying the Invention

'X' document of particular relevance; the claimed Invention cannot be considered novel or cannot be considered to involve an Inventive step when the document is taken alone

'Y' document of particular relevance; the claimed Invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

'&' document member of the same patent family

Date of the actual completion of the international search

17 September 2003

Date of mailing of the International search report

24/09/2003

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Wagner, R

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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Y	WO 00 34317 A (ADAIR FIONA SUZANNE ;CARR FRANCIS JOSEPH (GB); HAMILTON ANITA ANNE) 15 June 2000 (2000-06-15) page 8 -page 9	2-31, 33-36
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 02/12566

Box I	Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

. This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
   because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.:   1, 32
   because they relate to parts of the International Application that do not comply with the prescribed requirements to such
   an extent that no meaningful International Search can be carried out, specifically:

   see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II	Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all
   searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment
   of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report
   covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is
   restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest   ☐ The additional search fees were accompanied by the applicant's protest.

                               ☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet (1)) (July 1998)

FURTHER INFORMATION CONTINUED FROM   PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1, 32

The scope of claim 1 is not clearly defined because the skilled person,
in the possession of an antibody, is not able to determine whether said
antibody has been modified in comparison to a possible parental antibody.

Present claim   32 relates to an extremely large number of possible
peptides, especially because the wording " created from the primary
sequence" includes the possibility of modifying the fragments.. Support
within the meaning of Article 6 PCT and/or disclosure within the meaning
of Article 5 PCT is to be found, however, for only a very small
proportion of the peptides. A meaningful search over the whole of the
claimed scope is impossible. Consequently, the search has been limited to
the subject-matter defined by claim 33.

The applicant's attention is drawn to the fact that claims, or parts of
claims, relating to inventions in respect of which no international
search report has been established need not be the subject of an
international preliminary examination (Rule 66.1(e) PCT). The, applicant
is advised that the EPO policy when acting as an International
Preliminary Examining Authority is normally not to carry out a
preliminary examination on matter which has not been searched. This is
the case irrespective of whether or not the claims are amended following
receipt of the search report or during any Chapter II procedure.

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